

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2004, 11:55:12 ; Search time 76 Seconds
(without alignments)
1531.705 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPNGSGEGAREPWP.....DTGGDTGVTETTSANVKTMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq 29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2156	100.0	412	3 AAB02854	Aab02854 Human G p
2	2149	99.7	412	3 AAY54145	Aay54145 Amino aci
3	2149	99.7	412	4 AAB68478	Aab68478 Amino aci
4	2149	99.7	412	4 AAB62652	Aab62652 Long form
5	2149	99.7	412	5 ABG30936	Abg30936 Human G p
6	2149	99.7	412	6 AAB81933	Abp81933 Human mot
7	2149	99.7	501	4 AAB65822	Aag65822 Human GPR
8	2135	99.0	412	5 AAB09535	Aab09535 Human mot
9	1741	80.8	400	4 AAB68477	Aab68477 Amino aci
10	1575	73.1	386	3 AAY54146	Aay54146 Amino aci
11	1575	73.1	386	4 AAB62653	Aab62653 Short for
12	1143.5	53.0	271	4 AAB68476	Aab68476 Amino aci
13	901	41.8	363	3 AAY54147	Aay54147 The pufte
14	901	41.8	363	4 AAB68479	Aab68479 Amino aci
15	864.5	40.1	366	7 AAY90666	Aay90666 Human mut
16	864.5	40.1	366	7 ADC22729	Adc22729 Human G p
17	859.5	39.9	349	3 AAY69293	Aay69293 A. canine
18	857.5	39.8	366	3 AAY70345	Aay70345 Human G p
19	857.5	39.8	366	3 AAY90632	Aay90632 Human G p
20	857.5	39.8	366	4 AAB97376	Aab97376 Rat growt
21	857.5	39.8	366	4 AAB62650	Aab62650 Human G-p
22	857.5	39.8	366	5 ABB09534	Abb09534 Human ghr
23	857.5	39.8	366	7 ADC22607	Adc22607 Human G p
24	857.5	39.8	366	8 ADD35398	Add35398 Human gro
25	857	39.7	353	2 AAW19215	Aaw19215 Swine gro

26	857	39.7	353	2 AAW19608	Aaw19608 Pig growt
27	855.5	39.7	364	3 AAY54565	Aay54565 A mouse g
28	855.5	39.7	364	4 AAB97377	Aab97377 Rat growt
29	854	39.6	361	2 AAW19217	Aaw19217 Human gro
30	854	39.6	362	2 AAW19610	Aaw19610 Human gro
31	851.5	39.5	364	2 AAW19613	Aaw19613 Rat growt
32	839.5	38.9	364	2 AAW19220	Aaw19220 Rat growt
33	668.5	31.0	271	2 AAW19219	Aaw19219 Human gro
34	668.5	31.0	271	2 AAW19612	Aaw19612 Human gro
35	638.5	29.6	289	2 AAW19611	Aaw19611 Human gro
36	638.5	29.6	289	2 AAB81828	Abp81828 Human gro
37	635	29.5	289	2 AAW19216	Aaw19216 Swine gro
38	635	29.5	289	2 AAW19609	Aaw19609 Pig growt
39	633.5	29.4	289	2 AAW19218	Aaw19218 Human gro
40	498	23.1	418	4 ABB56371	Abb56371 Non-endog
41	495	23.0	418	2 AAR98562	Aar98562 Human neu
42	491	22.8	418	6 AAB81861	Abp81861 Human neu
43	491	22.8	542	4 ABG12316	Abg12316 Novel hum
44	490.5	22.8	403	3 AAY90673	Aay90673 Human mut
45	490.5	22.8	403	5 ABG95171	Abg95171 Human GPC

ALIGNMENTS

RESULT 1

AAB02854

ID AAB02854 standard; protein; 412 AA.

XX AC AAB02854;

XX DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor hGPR38

XX KW Human; G protein coupled receptor hGPR38 (V297K) protein SEQ ID NO:130.

KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.

OS Homo sapiens.

OS Synthetic.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US024065.

XX PR 13-OCT-1998; 98US-00170496.

XX PR 12-NOV-1998; 98US-0108029P.

XX PR 20-NOV-1998; 98US-0109213P.

XX PR 27-NOV-1998; 98US-0110060P.

XX PR 16-FEB-1999; 99US-0120416P.

XX PR 26-FEB-1999; 99US-0121852P.

XX PR 12-MAR-1999; 99US-0123944P.

XX PR 12-MAR-1999; 99US-0123945P.

XX PR 12-MAR-1999; 99US-0123946P.

XX PR 12-MAR-1999; 99US-0123948P.

XX PR 12-MAR-1999; 99US-0123949P.

XX PR 12-MAR-1999; 99US-0123951P.

XX PR 28-MAY-1999; 99US-0136436P.

XX PR 28-MAY-1999; 99US-0136437P.

XX PR 28-MAY-1999; 99US-0136439P.

XX PR 28-MAY-1999; 99US-0137127P.

XX PR 28-MAY-1999; 99US-0137131P.

XX PR 28-MAY-1999; 99US-0137567P.

XX PR 29-JUN-1999; 99US-0141448P.

XX PR 27-AUG-1999; 99US-0151114P.

XX PR 03-SEP-1999; 99US-0152524P.

XX PR 29-SEP-1999; 99US-0156555P.

XX PR 29-SEP-1999; 99US-0156633P.

XX PR 29-SEP-1999; 99US-0156634P.

XX PR 29-SEP-1999; 99US-0156653P.

XX PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157283P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.
 XX (AREN-) ARENA PHARM INC.
 XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
 XX WPI; 2000-317986/27.
 DR N-PSDB; AAA46116.
 XX Non-endogenous, human G protein-coupled receptors for screening receptor,
 PT inverse or partial agonists useful as therapeutic agents.
 XX Example 2; Page 168-169; 187pp; English.
 XX The present invention describes transmembrane receptors, preferably human
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is
 CC unknown (orphan GPCR receptors). More specifically the present invention
 CC relates to non-endogenous, constitutively activated versions of a human
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct
 CC identification of candidate compounds as receptors agonists, inverse
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
 CC exemplification of the present invention
 XX Sequence 412 AA;

Query Match 100.0%; Score 2156; DB 3; Length 412;
 Best Local Similarity 100.0%; Pred. No. 1.8e-194;
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60
 DB 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60
 QY 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVWFGPLLCRLSLYVGE 120
 DB 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVWFGPLLCRLSLYVGE 120
 QY 121 CTYATLLHMTALSVERYLAICRPLRARVLTTRRVRLIAVLMAVALLSAGPFLVGE 180
 DB 121 CTYATLLHMTALSVERYLAICRPLRARVLTTRRVRLIAVLMAVALLSAGPFLVGE 180
 QY 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240
 DB 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240
 QY 241 QLGAIRVLMWTTAYFFLPFTCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKVL 300
 DB 241 QLGAIRVLMWTTAYFFLPFTCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKVL 300
 QY 301 LVVLAFTICMLPHVGRRIIYNTEDSRMVFQSFVNIVALQLFVLSASINPILYNLISK 360
 DB 301 LVVLAFTICMLPHVGRRIIYNTEDSRMVFQSFVNIVALQLFVLSASINPILYNLISK 360
 QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGVTETTSANYKTWG 412
 DB 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGVTETTSANYKTWG 412

RESULT 2

AA54145

ID AA54145 standard; protein; 412 AA.

XX AC AA54145;

XX DT 27-MAR-2000 (first entry)

XX

DE Amino acid sequence of the motilin receptor splice variant MTL-R1A.
 XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;
 KW spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;
 KW functional defect; neurological disorder; scleroderma; colonoscopy;
 KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;
 KW infection; stress-related motility disorder; psychogenic disorder;
 KW gastroparesis; gastro-oesophageal reflux disease; constipation;
 KW chronic idiopathic pseudo obstruction; acute faecal impaction;
 KW postoperative ileus; gallstones; infantile colic; diarrhoea;
 KW irritable bowel syndrome; non-ulcer dyspepsion; non-cardiac chest pain;
 KW endoscopy; duodenal intubation.
 XX Homo sapiens.
 OS WO9964436-A1.
 XX 16-DEC-1999.
 PD 08-JUN-1999; 99WO-US012773.
 PF 12-JUN-1998; 98US-0089098P.
 PR (MERI) MERCK & CO INC.
 XX Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;
 PI Pong S, Smith RG;
 XX WPI; 2000-105868/09.
 DR N-PSDB; AAZ45403.
 XX Novel receptor protein for screening compounds used in treating irritable
 PT bowel syndrome, constipation and other gastric conditions.
 XX Claim 3; Fig 3; 44pp; English.

The present sequence represents splice variant MTL-R1A of the motilin
 receptor. The gene encodes a G-protein coupled receptor, and is
 designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A
 (see AA54145) and MTL-R1B (see AA54146). MTL-R1A is a functional seven
 transmembrane domain form, and MTL-R1B is a truncated five transmembrane
 domain. The MTL-R1 proteins are used to identify agonists and antagonists
 which can be used for treating gastric motility disorders, functional
 defects, disorders secondary to neurological disorders e.g. scleroderma,
 paraneoplastic syndromes radiation induced dysmotility, diabetes,
 infections, stress-related motility disorders, psychogenic disorders,
 gastroparesis, gastro-oesophageal reflux disease, constipation, chronic
 idiopathic pseudo obstruction, acute faecal impaction, postoperative
 ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer
 dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used
 CC in the preparation for colonoscopy, endoscopy and duodenal intubation
 CC

SQ Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 3; Length 412;
 Best Local Similarity 99.8%; Pred. No. 8.4e-194;
 Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60
 DB 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60
 QY 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVWFGPLLCRLSLYVGE 120
 DB 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVWFGPLLCRLSLYVGE 120
 QY 121 CTYATLLHMTALSVERYLAICRPLRARVLTTRRVRLIAVLMAVALLSAGPFLVGE 180
 DB 121 CTYATLLHMTALSVERYLAICRPLRARVLTTRRVRLIAVLMAVALLSAGPFLVGE 180
 QY 181 QDPGISVVGGLNGTARIASSPPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240
 DB 181 QDPGISVVGGLNGTARIASSPPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240

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QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRGHRQTKVYL 300
AAB68478
DB 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRGHRQTKVYL 300
QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQOLFYLASINPILYNLISK 360
DB 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQOLFYLASINPILYNLISK 360
QY 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVYTETTSANVKTMG 412
DB 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVYTETTSANVKTMG 412

RESULT 3
AAB68478
ID AAB68478 standard; protein; 412 AA.
XX AC AAB68478;
XX DT 23-JUL-2001 (first entry)
XX DE Amino acid sequence of a human motilin receptor polypeptide.
XX KW Motilin receptor; gastrointestinal disease; gastric motility disorder;
XX KW Gastroparesis; irritable bowel syndrome; diarrhoea.
XX OS Homo sapiens.
XX PN WO200132710-A1.
XX PD 10-MAY-2001.
XX PF 25-OCT-2000; 2000WO-US029426.
XX PR 29-OCT-1999; 99US-0162264P.
XX PA (MERI ) MERCK & CO INC.
XX PI Tan C, McKee K;
XX DR WPI; 2001-343479/36.
XX DR N-PSDB; AAF85449.
XX PT Novel polypeptides related to dog and rabbit motilin receptor
PT polypeptide, comprising unique regions from dog and motilin receptor
PT amino acid sequence, useful for identifying compounds for treating
PT diarrhea in humans.
XX PS Disclosure; Page 32-33; 42pp; English.
XX CC The present sequence represents a human motilin receptor polypeptide. The
CC specification describes an unique sequence present in exon 1 of the dog
CC motilin receptor, which is not present in human or Sphaeroides nephelus
CC 75E7 motilin receptor sequences. The unique nucleic acid sequence is
CC useful for measuring the ability of a compound to affect motilin receptor
CC activity. Motilin receptor polynucleotides and polypeptides are used to
CC identify therapeutic compounds which are useful for treating
CC gastrointestinal diseases and disorders such as gastric motility
CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea
XX SQ Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 4; Length 412;
Best Local Similarity 99.8%; Pred. No. 8.4e-194;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWALPCCDERCSPPPLGALVPVAVCLCLFVVGSGNVVTV 60
DB 1 MGSPWNGSDGEGAREPPWALPCCDERCSPPPLGALVPVAVCLCLFVVGSGNVVTV 60
QY 61 MLIGRYDRMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLCLSLYVGE 120
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DB 61 MLIGRYDRMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLCLSLYVGE 120
QY 121 CTYATLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAI WVALLSAGPFLFLVGVE 180
DB 121 CTYATLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAI WVALLSAGPFLFLVGVE 180
QY 181 QDPGISVVPGLNGTARTIASSPLASPPPLWLSRAPPPSPSPETAATAAALFSRECRPSPA 240
DB 181 QDPGISVVPGLNGTARTIASSPLASPPPLWLSRAPPPSPSPETAATAAALFSRECRPSPA 240
QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRGHRQTKVYL 300
DB 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRGHRQTKVYL 300
QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQOLFYLASINPILYNLISK 360
DB 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQOLFYLASINPILYNLISK 360
QY 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVYTETTSANVKTMG 412
DB 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVYTETTSANVKTMG 412

RESULT 4
AAB62652
ID AAB62652 standard; protein; 412 AA.
XX AC AAB62652;
XX DT 23-JUL-2001 (first entry)
XX DE Long form of motilin receptor, GPR-38A isoform.
XX KW zsig33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform.
XX OS Homo sapiens.
XX PN WO200138355-A2.
XX PD 31-MAY-2001.
XX PF 22-NOV-2000; 2000WO-US032074.
XX PR 22-NOV-1999; 99US-0166765P.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX WPI; 2001-355879/37.
XX DR N-PSDB; AAF83683.
XX PT Forming reversible peptide receptor complex for purifying cell and
PT peptides, stimulating signal transduction and modulating hormone
PT secretion, involves contacting a receptor with zsig33 polypeptide.
XX PS Disclosure; Page 102-104; 111pp; English.
XX CC The invention relates to a method of forming a reversible peptide-
XX receptor complex that involves providing an immobilized receptor, and
XX contacting the receptor with a zsig33 peptide (comprising residues 24-37
XX of AAB62649), where the receptor binds to the zsig33 peptide. The method
XX is useful for purifying cells, purifying a peptide, stimulating signal
XX transduction in a cell expressing a receptor. It is also useful for
XX modulating secretion of hormones, neural development and/or utilization,
XX gastric contractility, nutrient uptake, secretion of digestive and
XX pancreatic enzymes and hormones, secretion of insulin-like growth factor
XX -I, secretion of non-zsig33 proteins. It is useful for modulating growth
XX hormone secretion in a mammal having a disease associated with abnormal
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CC levels of growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, skeletal dysplasia, immune suppression, obesity, growth retardation, protein catabolic responses after surgery, cachexia, protein loss, dwarfism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety regulation, glucose absorption and metabolism and neuropathy-associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the long form of motilin receptor, GPR-38A (one of the two isoforms of GPR38 which result from alternative splicing). GPR38 has homology to the human G-protein coupled receptor, GHS-R

XX
SQ Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 4; Length 412;
Best Local Similarity 99.8%; Pred. No. 8.4e-194;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVCLCLFVVGVSGNVTV 60
Db 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVCLCLFVVGVSGNVTV 60

Qy 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCLRLSLYVGE 120
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCLRLSLYVGE 120

Qy 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLMAVALLSAGPFLVLGVE 180
Db 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLMAVALLSAGPFLVLGVE 180

Qy 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPSPPGPETAEEAALFSRECRPSPA 240
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPSPPGPETAEEAALFSRECRPSPA 240

Qy 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKRVL 300
Db 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKRVL 300

Qy 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360
Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360

Qy 361 KYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGDTVGVTETSANVKTWG 412
Db 361 KYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGDTVGVTETSANVKTWG 412

RESULT 5
ABG30936
XX
AC ABG30936;
XX
DT 21-OCT-2002 (first entry)
DE
DE Human G protein-coupled receptor 38 (GPR38).
XX
KW Human; G protein-coupled receptor 38; receptor; GPR38;
KW Alzheimer's disease; Parkinson's disease; ulcerative colitis;
KW Crohn's disease; Hodgkin's disease; glioblastoma; breast carcinoma;
KW colon carcinoma; lung small cell carcinoma; lung adenocarcinoma;
KW pancreatic small cell carcinoma; pancreatic adenocarcinoma.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT Region
FT Region
FT Region
FT Region

Location/Qualifiers
15..31
/note= "Antigenic fragment"
217..232
/note= "Antigenic fragment"
276..291
/note= "Antigenic fragment"

FT Region 373..388
/note= "Antigenic fragment"

XX WO200257791-A2.
FN 25-JUL-2002.
XX 29-NOV-2001; 2001WO-US045219.
XX 29-NOV-2000; 2000US-0250251P.
PR 30-NOV-2000; 2000US-0250452P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Brown JP, Burmer GC, Roush CL, Kulander BG;
XX WPI; 2002-566812/60.
DR N-PSDB; ABK90132.
XX Assay for detecting Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma or carcinoma, comprises using a binding partner for G protein coupled receptor 38.
XX Disclosure; Fig 2; 112pp; English.
XX The present invention relates to a new assay method that involves contacting a binding partner specific for G protein coupled receptor (GPR) 38 with specific cells. The method of the invention is useful for the detection of an increased risk of Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma, or carcinoma. GPR 38 is used to manufacture a medicament for inhibiting, treating or preventing Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma, breast carcinoma, colon carcinoma, lung small cell carcinoma, lung adenocarcinoma, pancreatic small cell carcinoma, and pancreatic adenocarcinoma. An agonist or antagonist to GPR 38 are used to manufacture a medicament able to reduce the symptoms of these diseases. Nucleic acids encoding GPR 38 can also be used to treat the diseases. The present amino acid sequence represents the human G protein-coupled receptor 38 (GPR38) of the invention

XX
SQ Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 5; Length 412;
Best Local Similarity 99.8%; Pred. No. 8.4e-194;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVCLCLFVVGVSGNVTV 60
Db 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVCLCLFVVGVSGNVTV 60

Qy 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCLRLSLYVGE 120
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCLRLSLYVGE 120

Qy 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLMAVALLSAGPFLVLGVE 180
Db 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLMAVALLSAGPFLVLGVE 180

Qy 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPSPPGPETAEEAALFSRECRPSPA 240
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPSPPGPETAEEAALFSRECRPSPA 240

Qy 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKRVL 300
Db 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKRVL 300

Qy 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360
Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360

Qy 361 KYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGDTVGVTETSANVKTWG 412
Db 361 KYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGDTVGVTETSANVKTWG 412

Db 361 KYRAAFKLLARKSRPGFHRSDTAGEVAGDTGDTVGYTETSANVKTMG 412

RESULT 6

ABP81993
ID ABP81993 standard; protein; 412 AA.

AC ABP81993;

XX 04-MAR-2003 (first entry)

DT Human motilin receptor GPR38 protein SEQ ID NO:473.

DE
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related receptor; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hyperextension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX Homo sapiens.

OS W0200261087-A2.

PN 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

PR (LIFE-) LIFESPAN BIOSCIENCES INC.

PA Burmer GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

DR N-PSDB; ABZ42842.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the

CC exemplification of the present invention

XX Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 6; Length 412;
Best Local Similarity 99.8%; Pred. No. 8.4e-194;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWFPALPCDERRCSPPFLGALVPTAVCLCLFVVGVSGNNVTV 60

Db 1 MGSPWNGSDGEGAREPPWFPALPCDERRCSPPFLGALVPTAVCLCLFVVGVSGNNVTV 60

QY 61 MLIGRYDMETTTNLYLGSMAVSDLLILLGLPFDLYLWRSRPVFGPLLCRLSLYVGE 120

Db 61 MLIGRYDMETTTNLYLGSMAVSDLLILLGLPFDLYLWRSRPVFGPLLCRLSLYVGE 120

QY 121 CTVATLLHMTALSVERVIALCRPLARAVLTVRRVRALIAVLMVAVALLSAGPFLFLVGE 180

Db 121 CTVATLLHMTALSVERVIALCRPLARAVLTVRRVRALIAVLMVAVALLSAGPFLFLVGE 180

QY 181 QDGPISVVGINGTARTASSPPLWLSRAPPPSGPETAAALFSRECRSPA 240

Db 181 QDGPISVVGINGTARTASSPPLWLSRAPPPSGPETAAALFSRECRSPA 240

QY 241 QLGALRVMLWVTYAYFELPCLCLISLYLGLRELWSSRPLRGPAASGRGRGHRTVRVL 300

Db 241 QLGALRVMLWVTYAYFELPCLCLISLYLGLRELWSSRPLRGPAASGRGRGHRTVRVL 300

QY 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQFLYLSASINPILYNLISK 360

Db 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQFLYLSASINPILYNLISK 360

QY 361 KYRAAFKLLARKSRPGFHRSDTAGEVAGDTGDTVGYTETSANVKTMG 412

Db 361 KYRAAFKLLARKSRPGFHRSDTAGEVAGDTGDTVGYTETSANVKTMG 412

RESULT 7

AAG65822
ID AAG65822 standard; protein; 501 AA.

XX AAG65822;

XX 30-JAN-2002 (first entry)

XX Human GPR38 variant GPR38V polypeptide.

XX GPR38V; variant; antibacterial; cytostatic; analgesic; antiasthmatic;
KW anti-Parkinsonian; hypertensive; hypotensive; antidiabetic; osteopathic;
KW antiallergic; antimigraine; neuroleptic; nootropic; anticonvulsant;
KW antiulcer; antiemetic; cardiant; vaccine; human.

XX Homo sapiens.

OS W0200164836-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006277.

XX 01-MAR-2000; 2000US-00516315.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Elshourbagy N, Shabon U;

PI WPI; 2001-638956/73.

DR N-PSDB; AAI66989.

XX New human GPR38V polypeptide and polynucleotide, useful for treating e.g. bacterial, fungal, protozoal and viral infections, cancers or allergies, PT as vaccines, and for identifying agonists and antagonists potentially useful in therapy.

XX PS Claim 1; Page 26; 32pp; English.

XX CC This represents a human GPR38 variant (GPR38V) polypeptide. GPR38V can be

XX CC expressed by standard recombinant methodology. The polynucleotides and

XX CC polypeptides are used in the treatment of bacterial, fungal, protozoal

XX CC and viral infections, infections caused by HIV-1 or HIV-2, pain, cancers,

XX CC diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart

XX CC failure, hypertension, urinary retentions, osteoporosis, allergies,

XX CC ulcers, migraine, psychotic and neurological disorders, or dyskinesias.

XX CC They are also useful for identifying agonists and antagonists that are

XX CC potentially useful in therapy, as vaccines to induce immunological

XX CC response in a mammal. The polypeptides may also be used as immunogens to

XX CC produce antibodies immunospecific for the polypeptides, and to identify

XX CC membrane bound or soluble receptors

XX SQ Sequence 501 AA;

Query Match 99.7%; Score 2149; DB 4; Length 501;

Best Local Similarity 99.8%; Pred. No. 1.1e-193;

Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60

DB 90 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 149

QY 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPILLCRLSLYVGE 120

DB 150 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPILLCRLSLYVGE 209

QY 121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180

DB 210 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 269

QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

DB 270 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 329

QY 241 QLGLRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPFLGPAASGRGRHQTKEVL 300

DB 330 QLGLRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPFLGPAASGRGRHQTKEVL 389

QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360

DB 390 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 449

QY 361 KYRAAAFLLARKSRPRGFRHSDTAGEVAGDTGGDTVGVTETTSANVKTMG 412

DB 450 KYRAAAFLLARKSRPRGFRHSDTAGEVAGDTGGDTVGVTETTSANVKTMG 501

RESULT 8

ABB09535

ID ABB09535 standard; protein; 412 AA.

XX AC ABB09535;

XX AC ABB09535;

XX AC ABB09535;

DT 22-OCT-2002 (first entry)

DE Human motilin receptor.

XX Human; motilin receptor; appetite; food intake; agonist; analogue;

KW undernutrition; anorexia; cachexia; malignant disease; infection;

KW inflammatory disease; weight loss; antagonist; obesity; anorectic;

KW anabolic; ghrelin receptor homologue; receptor.

XX OS Homo sapiens.

XX FN WO200260472-A1.

XX PD 08-AUG-2002.

XX PF 31-JAN-2002; 2002WO-JP000765.

XX PR 31-JAN-2001; 2001JP-00024423.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Inui A, Asakawa A, Kaga T;

XX XX WPI; 2002-619206/66.

DR Remedies for diseases with hypo-nutrition status e.g. inappetence and

PT cachexia, containing ghrelin or its analogs including agonists and

PT antagonists.

XX PS Disclosure; Fig 1B; 50pp; Japanese.

XX CC The invention relates to the use of ghrelin or its analogues for the

XX CC treatment of diseases associated with undernutrition such as anorexia,

XX CC and also relates to the use of ghrelin antagonists for the prevention or

XX CC treatment of obesity. The invention additionally discloses a method for

XX CC screening ghrelin agonists or antagonists by measuring the amount of food

XX CC intake, neuropeptide Y (NPY) expression, binding of NPY to NPY receptor

XX CC Y1, oxygen consumption, gastric emptying, or activity of the vagus nerve.

XX CC Intracerebroventricular (icv) administration of ghrelin in animals was

XX CC found to increase food intake over a period of 24 hours. Ghrelin and its

XX CC analogues may therefore be used to treat conditions such as loss of

XX CC appetite, anorexia, cachexia, malignant diseases, and weight loss

XX CC associated with infection or inflammatory diseases. Conversely, ghrelin

XX CC antagonists may be used in the treatment of obesity. The present sequence

XX CC represents the human motilin receptor, a homologue of the ghrelin

XX CC receptor (AB09534) which is referred to in the disclosure of the

XX CC invention

XX SQ Sequence 412 AA;

Query Match 99.0%; Score 2135; DB 5; Length 412;

Best Local Similarity 99.3%; Pred. No. 1.8e-192;

Matches 409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60

DB 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60

QY 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPILLCRLSLYVGE 120

DB 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPILLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180

DB 121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180

QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

QY 241 QLGLRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPFLGPAASGRGRHQTKEVL 300

DB 241 QLGLRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPFLGPAASGRGRHQTKEVL 300

QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360

DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360

QY 361 KYRAAAFLLARKSRPRGFRHSDTAGEVAGDTGGDTVGVTETTSANVKTMG 412

DB 361 KYRAAAFLLARKSRPRGFRHSDTAGEVAGDTGGDTVGVTETTSANVKTMG 412

RESULT 9

AAB68477

ID AAB68477 standard; protein; 400 AA.

XX AC AAB68477;

XX AC AAB68477;

DT 23-JUL-2001 (first entry)
 XX Amino acid sequence of a rabbit motilin receptor polypeptide.
 KW Motilin receptor; gastrointestinal disease; gastric motility disorder;
 KW gastroparesis; irritable bowel syndrome; diarrhoea.
 OS Oryctolagus cuniculus.
 XX WO200132710-A1.
 FN 10-MAY-2001.
 XX 25-OCT-2000; 2000WO-US029426.
 XX 29-OCT-1999; 99US-0162264P.
 XX (MERI) MERCK & CO INC.
 XX Tan C, McKee K;
 XX WPI; 2001-343479/36.
 DR N-PSDB; AAF85448.
 XX Novel polypeptides related to dog and rabbit motilin receptor
 PT polypeptide, comprising unique regions from dog and motilin receptor
 PT amino acid sequence, useful for identifying compounds for treating
 PT diarrhea in humans.
 XX Claim 8; Page 18; 42pp; English.
 XX The present sequence represents a rabbit motilin receptor polypeptide.
 CC The specification describes a unique sequence present in exon 1 of the
 CC dog motilin receptor, which is not present in human or Sphaeroides
 CC nephelus 7567 motilin receptor sequences. The unique nucleic acid
 CC sequence is useful for measuring the ability of a compound to affect
 CC motilin receptor activity. Motilin receptor polynucleotides and
 CC polypeptides are used to identify therapeutic compounds which are useful
 CC for treating gastrointestinal diseases and disorders such as gastric
 CC motility disorders, gastroparesis, irritable bowel syndrome, and
 CC diarrhoea
 XX Sequence 400 AA;
 Query Match 80.8%; Score 1741; DB 4; Length 400;
 Best Local Similarity 83.7%; Pred. No. 2.3e-155;
 Matches 343; Conservative 11; Mismatches 44; Indels 12; Gaps 3;
 QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAACLCFLFVGVSGNVVTV 60
 DB 1 MGSPWNGSDGPEADAREPPWAALPPCDERRCSPFPLGLTVPTAVTAVGLFAVGVSGNVVTV 60
 QY 61 MLIGRYDMRTTNLYLGSMAVSDLLILGLPDLVRLWRSPVWPGLLCLSLVYVGG 120
 DB 61 LLIIGRYDMRTTNLYLGSMAVSDLLILGLPDLVRLWRSPVWPGLLCLSLVYVGG 120
 QY 121 CTYATLLHMTALSVRYLAICPLRLARVLVTRRRVALLAVALLSAGPFLVAVGE 180
 DB 121 CTYASLLHMTALSVRYLAICPLRLARVLVTRRRVALLAALVALLSAGPFLVAVGE 180
 QY 181 QPGISVWPLNGLTARIASSPLASSPPLWLSRAPPSPSGPETABAAALFSGRCRPSA 240
 DB 181 QDPAPVAAPDRNGTV-----PLDPSSP-----APASPPSGP-GAFAAALFSGRCRPSA 228
 QY 241 QLGARVLMVWVTAYTAYFLPLCLSLIYGLIGRLWSSRPLRGPAASGRGHRQTVRL 300
 DB 229 QGLLRVLMVWVTAYTAYFLPLCLSLIYGLIARGLRGPLRGPAATGRGHRQTVRL 288
 QY 301 LVVLAFLICWLPFFHVGRIIYINTEDSRMMYFSQYENIVALQLFYLSASINPILYNLSK 360
 DB 289 LVVLAFLICWLPFFHVGRIIYINTQSRMMYFSQYENIVALQLFYLSASINPILYNLSK 348
 QY 361 KYRAAAFKLLARKSRPRGFHRSRDTAGEVAGTGDGTGVYTTETSANVKT 410

DB 349 KYRAAARLLRSRAGPSVCGSROPEQDVAGDTGDTAGTETSANTKT 398
 RESULT 10
 AAY54146
 ID AAY54146 standard; protein; 386 AA.
 XX AAY54146;
 AC 27-MAR-2000 (first entry)
 XX Amino acid sequence of the motilin receptor splice variant MTL-R1B.
 DE Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;
 XX spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;
 KW functional defect; neurological disorder; scleroderma; colonoscopy;
 KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;
 KW infection; stress-related motility disorder; psychogenic disorder;
 KW gastroparesis; gastro-oesophageal reflux disease; constipation;
 KW chronic idiopathic pseudo obstruction; acute faecal impaction;
 KW postoperative ileus; gallstones; infantile colic; diarrhoea;
 KW irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;
 KW endoscopy; duodenal intubation.
 XX Homo sapiens.
 OS WO9964436-A1.
 XX 16-DEC-1999.
 XX 08-JUN-1999; 99WO-US012773.
 XX 12-JUN-1998; 98US-0089098P.
 XX (MERI) MERCK & CO INC.
 XX Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;
 PI Pong S, Smith RG;
 XX WPI; 2000-105868/09.
 DR N-PSDB; AA245404.
 XX Novel receptor protein for screening compounds used in treating irritable
 PT bowel syndrome, constipation and other gastric conditions.
 XX Claim 5; Fig 5; 44pp; English.
 XX The present sequence represents splice variant MTL-R1B of the motilin
 CC receptor. The gene encodes a G-protein coupled receptor, and is
 CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A
 CC (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a functional seven
 CC transmembrane domain form, and MTL-R1B is a truncated five transmembrane
 CC domain. The MTL-R1 proteins are used to identify agonists and antagonists
 CC which can be used for treating gastric motility disorders, functional
 CC defects, disorders secondary to neurological disorders e.g. scleroderma,
 CC paraneoplastic syndromes radiation induced dysmotility, diabetes,
 CC infections, stress-related motility disorders, psychogenic disorders,
 CC gastroparesis, gastro-oesophageal reflux disease, constipation, chronic
 CC idiopathic pseudo obstruction, acute faecal impaction, postoperative
 CC ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer
 CC dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used
 CC in the preparation for colonoscopy, endoscopy and duodenal intubation
 XX Sequence 386 AA;
 Query Match 73.1%; Score 1575; DB 3; Length 386;
 Best Local Similarity 99.7%; Pred. No. 9.9e-140;
 Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAACLCFLFVGVSGNVVTV 60
 DB 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAACLCFLFVGVSGNVVTV 60

QY 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLRLSLYVGE 120
 DB 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLRLSLYVGE 120
 QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLAVALLSAGPFLFLVGVE 180
 DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLAVALLSAGPFLFLVGVE 180
 QY 181 QDPCISVVGGLNGTARIASSPLASPPPLWLSRAPPPSPGPETAETAAALFSRECRPSPA 240
 DB 181 QDPCISVVGGLNGTARIASSPLASPPPLWLSRAPPPSPGPETAETAAALFSRECRPSPA 240
 QY 241 QLGALRVMLWVTYAFYFFLPFLCLSLYGLIGRELWSSRPPLRGPAASGRGRGHRTKRVL 300
 DB 241 QLGALRVMLWVTYAFYFFLPFLCLSLYGLIGRELWSSRPPLRGPAASGRGRGHRTKRVL 300

RESULT 11

AAB62653
 ID AAB62653 standard; protein; 386 AA.

AC AAB62653;

DT 23-JUL-2001 (first entry)

DE Short form of motilin receptor, GPR-38B isoform.

XX zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38B; isoform.

XX Homo sapiens.

XX WO200138955-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032074.

XX 22-NOV-1999; 99US-0166765P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

XX WPI; 2001-355879/37.

XX N-PSDB; AAF83684.

XX Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide.

XX Disclosure; Page 106-109; 11pp; English.

XX The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having

CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the short form of
 CC motilin receptor, GPR-38B (one of the two isoforms of GPR38 which result
 CC from alternative splicing). GPR38 has homology to the human G-protein
 CC coupled receptor, GHS-R

XX Sequence 386 AA;

Query Match 73.1%; Score 1575; DB 4; Length 386;

Best Local Similarity 99.7%; Pred. No. 9.9e-140;

Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPWPALPCDERRCSPFPALGVPTAVCLCLFVVGVSGNVVTV 60

DB 1 MGSPWNGSDGPEGAREPWPALPCDERRCSPFPALGVPTAVCLCLFVVGVSGNVVTV 60

QY 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLRLSLYVGE 120

DB 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLRLSLYVGE 120

QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLAVALLSAGPFLFLVGVE 180

DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLAVALLSAGPFLFLVGVE 180

QY 181 QDPCISVVGGLNGTARIASSPLASPPPLWLSRAPPPSPGPETAETAAALFSRECRPSPA 240

DB 181 QDPCISVVGGLNGTARIASSPLASPPPLWLSRAPPPSPGPETAETAAALFSRECRPSPA 240

QY 241 QLGALRVMLWVTYAFYFFLPFLCLSLYGLIGRELWSSRPPLRGPAASGRGRGHRTKRVL 300

DB 241 QLGALRVMLWVTYAFYFFLPFLCLSLYGLIGRELWSSRPPLRGPAASGRGRGHRTKRVL 300

RESULT 12

AAB68476

ID AAB68476 standard; protein; 271 AA.

AC AAB68476;

XX 23-JUL-2001 (first entry)

XX Amino acid sequence of a dog motilin receptor exon 1.

XX Motilin receptor; gastrointestinal disease; gastric motility disorder;
 KW gastroparesis; irritable bowel syndrome; diarrhoea.

XX Canis sp.

XX WO200132710-A1.

XX 10-MAY-2001.

XX 25-OCT-2000; 2000WO-US029426.

XX 29-OCT-1999; 99US-0162264P.

XX (MERI) MERCK & CO INC.

XX Tan C, McKee K;

XX WPI; 2001-343479/36.

XX N-PSDB; AAF85447.

XX Novel polypeptides related to dog and rabbit motilin receptor
 PT polypeptide, comprising unique regions from dog and motilin receptor
 PT amino acid sequence, useful for identifying compounds for treating
 PT diarrhea in humans.

XX Claim 4; Page 17; 42pp; English.

XX The present sequence is encoded by exon 1 of a dog motilin receptor gene.

CC The specification describes an unique sequence present in exon 1 of the
 CC motilin receptor, which is not present in human or Spherooides nephelus
 CC 75E7 motilin receptor sequences. The unique nucleic acid sequence is
 CC useful for measuring the ability of a compound to affect motilin receptor
 CC activity. Motilin receptor polynucleotides and polypeptides are used to
 CC identify therapeutic compounds which are useful for treating
 CC gastrointestinal diseases and disorders such as gastric motility
 CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea
 XX
 XX Sequence 271 AA;

Query Match 53.0%; Score 1143.5; DB 4; Length 271;
 Best Local Similarity 76.7%; Pred. No. 3e-99;
 Matches 230; Conservative 13; Mismatches 28; Indels 29; Gaps 4;
 QY 1 MGSFNGSDGPEGARPPHPALPCDERCSPPLGALVPVTAVCICLVGVGSGNVTV 60
 Db 1 MGGPGNSDGAEGAQ-----LPCDERLCSPPLGALVPVTAVCICLVGVGSGNLTV 53
 QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPVFGPLLCRLSLYVGEG 120
 Db 54 LLIGRYDRMTTNNLYLGSMAVSDLLILGLPDLRLWRSRPVFGPLLCRLSLYVGEG 113
 QY 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVALLAVLWAVALLSAGPFLVLVGE 180
 Db 114 CYATLLHVTALSVERYLAICRPLRARVLLRRRARALLSRAVALLSAAFPFLVLVGE 173
 QY 181 ODPGISVPLGNGTARIASSPLASSPPLWSRAPPSPGPGTAAALFRCRPSPA 240
 Db 174 QDAG---GFLNGSARLAA-----PSPPGPGP---AALFRCRCPSPS 211
 QY 241 QLGALRVMLWVTTAYFPFLFCLISLYGLIGRELWSSRPLRGPAASGRGHRQTKVYL 300
 Db 212 QLGALRVMLWVTTAYFPFLFCLISLYGLIGRELWSSRPLRGPAASGRGHRQTKVYL 271

RESULT 13
 AAY54147
 ID AAY54147 standard; protein; 363 AA.
 XX
 AC AAY54147;
 XX
 DT 12-SEP-2003 (revised)
 DT 27-MAR-2000 (first entry)
 XX
 DE The puffer fish motilin receptor protein encoded by clone 75E7.
 XX
 KW Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;
 KW spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;
 KW functional defect; neurological disorder; scleroderma; colonoscopy;
 KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;
 KW infection; stress-related motility disorder; psychogenic disorder;
 KW gastroparesis; gastro-oesophageal reflux disease; constipation;
 KW chronic idiopathic pseudo obstruction; acute faecal impaction;
 KW postoperative ileus; gallstones; infantile colic; diarrhoea;
 KW irritable bowel syndrome; non-ulcer dyspepsion; non-cardiac chest pain;
 KW endoscopy; duodenal intubation.

OS Spherooides nephelus.
 XX
 XX WO9964436-A1.
 XX
 PD 16-DEC-1999.
 XX
 PF 08-JUN-1999; 99WO-US012773.
 XX
 PR 12-JUN-1998; 98US-0089098P.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 XX Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;
 PI Pong S, Smith RG;

DR WPI; 2000-105868/09.
 DR N-PSDB; AAZ45405.
 XX
 PT Novel receptor protein for screening compounds used in treating irritable
 PT bowel syndrome, constipation and other gastric conditions.
 XX
 PS Claim 7; Fig 8; 44pp; English.

XX
 CC The present sequence represents a motilin receptor (clone 75E7) which is
 CC related to the human motilin receptor of the invention. The specification
 CC describes a G-protein coupled receptor, designated MTL-R1 (also GPR38).
 CC Two spliced forms of GPR38 exist, MTL-R1A (see AAY54145) and MTL-R1B (see
 CC AAY54146). MTL-R1A is a functional seven transmembrane domain form, and
 CC MTL-R1B is a truncated five transmembrane domain. The MTL-R1 proteins are
 CC used to identify agonists and antagonists which can be used for treating
 CC gastric motility disorders, functional defects, disorders secondary to
 CC neurological disorders e.g. scleroderma, paraneoplastic syndromes
 CC radiation induced dysmotility, diabetes, infections, stress-related
 CC motility disorders, psychogenic disorders, gastroparesis, gastro-
 CC oesophageal reflux disease, constipation, chronic idiopathic pseudo
 CC obstruction, acute faecal impaction, postoperative ileus, gallstones,
 CC infantile colic, irritable bowel syndrome, non-ulcer dyspepsion, non-
 CC cardiac chest pain and diarrhoea. They can also be used in the
 CC preparation for colonoscopy, endoscopy and duodenal intubation. (Updated
 CC on 12-SEP-2003 to standardise OS field)

XX Sequence 363 AA;

Query Match 41.8%; Score 901; DB 3; Length 363;
 Best Local Similarity 50.3%; Pred. No. 3.1e-76;
 Matches 179; Conservative 56; Mismatches 77; Indels 44; Gaps 5;
 QY 31 SPFGALVPVTAVCICLVGVGSGNVTVMLIGRYDRMTTNNLYLGSMAVSDLLILG 90
 Db 31 SLFPASTLIPVTVICILIFVVGVTGNTWTLIIQYFKDMKTTNNLYLSSMAVSDLVIFLC 90
 QY 91 LPFDLYRLWRSRPVFGPLLCRLSLYVGEGCTYALLHMTALSVERYLAICRPLRARVL 150
 Db 91 LPFDLYRLWKYVPVLFGEAVCLVHYIFEGCTSATILHITLALSIBRYLAISFPLRSKMV 150
 QY 151 TRRRVRLIALVAVALLSAGPFLVLGVGQDPG;SVVPLGNGTARIASSPLASSPPLML 210
 Db 151 TRRRVQYIILALWCALVSAPTFLVGVGYD-----NET----- 185
 QY 211 SHAPPPSPGPGTAAALFRCRPSPAQL--GALRVMLWVTTAYFPFLFCLISLYG 268
 Db 186 ----HPDYN TG-----QCKHTGYA;SSGQLHIMVWSTTYFPCPMLCLFLYG 229
 QY 269 LTGRELWSSRPLRGPAASGRGHRQTKVLLVTVLAFILICWLPFHVGRIIYINTEDSR 328
 Db 230 SIGCKLWKSNDLQGPCALARESHRQTKVLLVTVLAFILICWLPYHIGRN;FAQVDDYD 289
 QY 329 MMVFSQYFNIVALQLFYLSASINPILYNLISKYRAAFAKLLARKSRGPRGHRSR 384
 Db 290 TAMLSONFNMAWMVLCYLSASINPVVYNLMSKYRAAARLLELHQ-RPKPAHRGQ 344

RESULT 14
 AAB68479
 ID AAB68479 standard; protein; 363 AA.
 XX
 AC AAB68479;
 XX
 DT 06-AUG-2003 (revised)
 DT 23-JUL-2001 (first entry)
 XX

DE Amino acid sequence of a motilin receptor polypeptide.
 XX
 KW Motilin receptor; gastrointestinal disease; gastric motility disorder;
 KW gastroparesis; irritable bowel syndrome; diarrhoea.
 XX
 OS Spherooides nephelus.

PN WO200132710-A1.
XX 10-MAY-2001.
XX 25-OCT-2000; 2000WO-US029426.
XX 29-OCT-1999; 99US-0162264P.
XX (MERI) MERCK & CO INC.
XX Tan C, McKee K;
XX WPI; 2001-343479/36.
XX N-PSDB; AAF85450.
XX Novel polypeptides related to dog and rabbit motilin receptor
XX polypeptide, comprising unique regions from dog and motilin receptor
XX amino acid sequence, useful for identifying compounds for treating
XX diarrhea in humans.
XX Disclosure; Page 33-34; 42pp; English.
XX The present sequence represents a bacterial motilin receptor polypeptide.
XX The specification describes a unique sequence present in exon 1 of the
XX dog motilin receptor, which is not present in human or Sphaeroides
XX nepheus 75E7 motilin receptor sequences. The unique nucleic acid
XX sequence is useful for measuring the ability of a compound to affect
XX motilin receptor activity. Motilin receptor polynucleotides and
XX polypeptides are used to identify therapeutic compounds which are useful
XX for treating gastrointestinal diseases and disorders such as gastric
XX motility disorders, gastroparesis, irritable bowel syndrome, and
XX diarrhoea. (Updated on 06-AUG-2003 to correct OS field.)
XX Sequence 363 AA;
SQ
Query Match 41.8%; Score 901; DB 4; Length 363;
Best Local Similarity 50.3%; Pred. No. 3.1e-76;
Matches 179; Conservative 56; Mismatches 77; Indels 44; Gaps 5;
QY 31 SPFGLGALVPYATVCLCLFVVGVSNNVTVMLIGYRDMRTTNLYLGSMAVSDLLILLG 90
Db 31 SLFPASTLIPVTVICILIFVVGVTGNTWTIIIOYFKDMKTTNLYLSSMAVSDLVIFLC 90
QY 91 LPFDLYLRWRSPVWFGPCLRLSLYVGEQCTYATLLHMTALSVERYLAICRPLARVLV 150
Db 91 LPFDLYLRWKVYVWMLFGEAVCRLYHYIEGCTSAITLHITALSERYLAISFPLRSKVMV 150
QY 151 TRRRVRLIALVAVALLSAGPFLVGVQDPGIVGVPLNGTARIASSPLASSPPLWL 210
Db 151 TRRRVQYIILALWCALVSAAPTFLVGVQD-----NET----- 185
QY 211 SRAPPPSPSPGPTAEAAALFSRECRPSAOL--GALRVMLVWTTTAYFPLFLCLSLIYLG 268
Db 186 ---HPDYNIG-----QCKHTGYAISGQLHIMVSTTYFCFMCMLCLLYG 229
QY 269 LIGELWSSRRPLRGPAAASGRGHRQKRVLLVVLVLAFFICWLPFFHVGRIIYINTEDSR 328
Db 230 SIGCKLWKSNDLQGPCALARSHRQVTKLVVVLVLAFFICWLPYHIGRNLFQAQVDYD 289
QY 329 MMYSQVENIVALQIFYLASINPILYNLSKYPAAAFKILLAKRSRPGFHRSR 384
Db 290 TAMLSONFMASVLCYLSASINPVVYVNLNGKRYAAAKRLLHQ--RPKPAHRGQ 344
RESULT 15
RAY90666
ID AAY90666 standard; protein; 366 AA.
XX AAY90666;
XX AAY90666;
XX 21-AUG-2000 (first entry)
XX Human mutant G protein-coupled receptor GHSR (V262K).
DE

XX G protein-coupled receptor; GPCR; constitutively active;
XX intracellular loop 3; transmembrane domain 6; drug screening; agonist;
XX antagonist; mutant; mutein.
XX Homo sapiens.
XX Synthetic.
XX WO200022129-A1.
XX 20-APR-2000.
XX 12-OCT-1999; 99WO-US023938.
XX 13-OCT-1998; 98US-00170496.
XX (AREN-) ARENA PHARM INC.
XX Behan DP, Chalmers DT, Liaw CW;
XX WPI; 2000-329165/28.
XX N-PSDB; AAA30732.
XX Non-endogenous constitutively activated human G protein-coupled
XX receptors, useful for identifying agonists for use as pharmaceutical
XX agents.
XX Example 2; Page 267-268; 34pp; English.
XX The invention relates to constitutively active, non-endogenous versions
XX of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
XX AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
XX and AAA30775-A30779). The mutant proteins of the invention contain a
XX mutation in a portion of the protein comprising intracellular loop 3
XX (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
XX is substituted for an endogenous residue in IC3 at a position 16 amino
XX acids N-terminal of an endogenous proline in TM6 to form a sequence X-
XX (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
XX Ala, and is preferably Lys. When the endogenous residue at this position
XX is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
XX amino acid stretch between the substituted amino acid and the Pro may be
XX endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
XX residues. The constitutively active GPCRs are useful for identifying
XX antagonists, agonists and partial agonists for use as pharmaceutical
XX agents. The mutant proteins are also useful in research settings for
XX elucidating the roles of the receptors in normal and diseased conditions.
XX Antagonists for a particular GPCR are useful for treating diseases and
XX disorders associated with that receptor. Because the novel mutant GPCRs
XX are constitutively active, they can be used directly for screening of
XX compounds without the need for endogenous ligands. Sequences AAY90643-
XX AAY90677 and AAY90683-Y90687 the mutant human GPCRs of the invention
XX Sequence 366 AA;
SQ
Query Match 40.1%; Score 864.5; DB 3; Length 366;
Best Local Similarity 44.7%; Pred. No. 8.7e-73;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;
QY 5 WNGSDGEGA-----REPPWPAALPPCD---ERRCSPPLGALVPTAVCLFVVGSGN 56
Db 2 WNATPSEPFGNLTADLDWDASGNDLSGDELLQLFPAPLLAGVTATCTVALFVVGAGN 61
QY 57 VVTMLIGRYDMRTTNLYLGSMAVSDLLILLGLPELYLRWRSPVWFGPFLICRLSLY 116
Db 62 LITMLVSVSRFRLEKTTNLYLSSMAVSDLLIFLCMPDLJDLVRLWQYRPNWFGDLLCKLFQF 121
QY 117 VGECTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIALVAVALLSAGPFLFL 176
Db 122 VSECTATVLTALSVERYFALCFPLRAKVTVTKGRVTVVAVAFCSAGPFLVL 181
QY 177 VGVQDPGIVGVPLNGTARIASSPLASSPPLMLSRAPPPSPGPTAEAAALFSRECR 236
Db 182 VGVHE-----NGT-----DP--W-----DTNECR 199

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OM protein - protein search, using sw model

Run on: July 4, 2004, 03:07:53 ; Search time 23 Seconds
(without alignments)
924.778 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPWNGSDGEGAREPPWPDTGSDTVGYTETSANVKTWG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
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3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/6C_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/6D_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2149	99.7	412	4	US-09-743-742B-8
2	864.5	40.1	366	4	US-09-170-496D-210
3	859.5	39.9	349	4	US-09-762-661A-2
4	858.5	39.8	366	4	US-09-762-661A-7
5	858.5	39.8	366	4	US-09-743-475-6
6	857.5	39.8	366	3	US-09-743-475-6
7	857.5	39.8	366	4	US-09-077-674-13
8	857.5	39.8	366	4	US-09-170-496D-88
9	857.5	39.8	366	4	US-09-743-742B-7
10	857.5	39.8	366	4	US-09-762-661A-5
11	857.5	39.8	366	4	US-09-364-425B-45
12	857.5	39.8	366	4	US-09-743-475-4
13	857	39.7	353	3	US-09-077-675A-3
14	857	39.7	353	4	US-09-077-674-3
15	855.5	39.7	364	3	US-09-077-675A-16
16	855.5	39.7	364	4	US-09-077-674-16
17	855.5	39.7	364	4	US-09-762-661A-6
18	855.5	39.7	364	4	US-09-743-475-3
19	855.5	39.7	364	4	US-09-743-475-5
20	854	39.6	361	3	US-09-077-675A-8
21	854	39.6	361	4	US-09-077-674-8
22	769.5	35.7	302	3	US-09-077-675A-2
23	769.5	35.7	302	4	US-09-077-674-2
24	768.5	35.6	302	3	US-09-077-675A-7
25	768.5	35.6	302	4	US-09-077-674-7
26	668.5	31.0	271	3	US-09-077-675A-12
27	668.5	31.0	271	4	US-09-077-674-12

28	638.5	29.6	289	3	US-09-077-675A-10	Sequence 10, Appl
29	638.5	29.6	289	4	US-09-077-674-10	Sequence 10, Appl
30	627	29.1	289	3	US-09-077-675A-5	Sequence 5, Appl
31	627	29.1	289	4	US-09-077-674-5	Sequence 5, Appl
32	491	22.8	418	4	US-09-743-742B-5	Sequence 5, Appl
33	490.5	22.8	403	4	US-09-170-496D-224	Sequence 224, App
34	484.5	22.5	403	4	US-09-170-496D-114	Sequence 114, App
35	484.5	22.5	403	4	US-09-743-742B-4	Sequence 4, Appl
36	484.5	22.5	403	4	US-09-743-742B-10	Sequence 10, Appl
37	477	22.1	415	4	US-09-545-944-2	Sequence 2, Appl
38	463	21.5	353	1	US-08-118-270-45	Sequence 45, Appl
39	463	21.5	353	5	PCT-US93-08528-45	Sequence 45, Appl
40	456.5	21.2	405	4	US-09-743-742B-2	Sequence 2, Appl
41	456.5	21.2	405	4	US-09-743-742B-11	Sequence 11, Appl
42	407	18.9	410	3	US-08-858-876A-2	Sequence 2, Appl
43	407	18.9	410	3	US-09-472-880-2	Sequence 2, Appl
44	401	18.6	415	4	US-09-743-742B-6	Sequence 6, Appl
45	401	18.6	416	3	US-08-858-876A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-743-742B-8
; Sequence 8, Application US/09743742B
; Patent No. 6599718
; GENERAL INFORMATION:
; APPLICANT: Liu, Qingyun
; APPLICANT: Howard, Andrew D.
; APPLICANT: McKee, Karen Kulju
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED
; TITLE OF INVENTION: RECEPTORS AND NUCLEIC ACIDS
; FILE REFERENCE: 20217YP
; CURRENT APPLICATION NUMBER: US/09/743,742B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: PCT/US99/15941
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: 60/092,623
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-743-742B-8

Query Match 99.7%; Score 2149; DB 4; Length 412;
Best Local Similarity 99.8%; Pred. No. 2.2e-175;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MGSPWNGSDGEGAREPPWPALPCDERRCSPFPPLGALVPTAVCLCLFVVGVSQNVTV 60	
DB	1	MGSPWNGSDGEGAREPPWPALPCDERRCSPFPPLGALVPTAVCLCLFVVGVSQNVTV 60	
QY	61	MLIGRYDMRTTNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPLCLSLYVGE 120	
DB	61	MLIGRYDMRTTNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPLCLSLYVGE 120	
QY	121	CTYATLHMTALSVERYLAI CRPLRVRVLRVRRVRIALVAVALLSAGPFLFVGE 180	
DB	121	CTYATLHMTALSVERYLAI CRPLRVRVLRVRRVRIALVAVALLSAGPFLFVGE 180	
QY	181	QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAAALFSRCRPSA 240	
DB	181	QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAAALFSRCRPSA 240	
QY	241	QLGALRVMLVTTAYFFLPFLCLSLYGLICRELWSSRRPLRGPAASGRGRHQTKEVL 300	
DB	241	QLGALRVMLVTTAYFFLPFLCLSLYGLICRELWSSRRPLRGPAASGRGRHQTKEVL 300	
QY	301	LVVVLAFTICWLPFHVGRIIYINTEDSRMVFQVFNVALQLFVLSASINPLYNLSK 360	

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Db 301 LVVLAFLICWLPVHGRIIIVNTSDSEMYFSQYFNIVALQLFYLASINPILYNLSK 360
QY 361 KYRAAAKFLLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTETTSANVKTWG 412
Db 361 KYRAAAKFLLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTETTSANVKTWG 412

RESULT 2
US-09-170-496D-210
; Sequence 210, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 210
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-210

Query Match 40.1%; Score 864.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 6e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPLGALVPVTAVCILCFVVGSGN 56
Db 2 WNAIPEEPGFNLTLADWDADSPGNSLGDLELLQLFPALLAGVTATCVAFVVGAGN 61
QY 57 VVTVMILGRYDRMTTNLYLGSMAYSDLLILGLPDLVRLWRSRPPWFGPPLLCLRLSLY 116
Db 62 LLETWLVSRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDILCKLFQF 121
QY 117 VGECTATILHMTALSVERYLAIICRPLARVLVTRRRVRLATVAVALLSAGPPLFL 176
Db 122 VSESCYATVLTITALSVERYFAICFPLRAKVLTKGRVKLVFVIWAVAFCSAGPIFVL 181
QY 177 VGVQDQPGISWVPLNGTARIASSPLASPPPLMLSRAPPPSGPPTAAALFSRECR 236
Db 182 VGVHE-----NGT-----DP-W-----DTNECR 199
QY 237 PS--PAQLGALRVMLVTTAYFFLPCLSLYLIGLIGRELWSSRRPLRGPAASGRGRGHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVCLTVLYSLIGRLKLRRRRGDAVVGASLRQNHK 259
QY 295 QTKRVLVVVLAFLICWLPVHGRIIIVNTSDS---RMMYFSQYFNIVALQLFYLASIN 351
Db 260 QTKRMIAVVVFAFLCWLPHVGRYLFKSPFSGLEIAIQSYCNLVSFVLYLSAAIN 319
QY 352 PILYNLSKKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTETTSAN 407
Db 320 PILYNMSKKYRVAVFELLGFEPFSQKLSLTKDESR-----AWTESSIN 365

RESULT 3
US-09-762-661A-2
; Sequence 2, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; TITLE OF INVENTION: RECEPTOR
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; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-762-661A-2
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Query Match 39.9%; Score 859.5; DB 4; Length 349;
Best Local Similarity 46.2%; Pred. No. 1.5e-65;
Matches 186; Conservative 50; Mismatches 98; Indels 69; Gaps 8;

QY 14 AREPP---WPALPPCDERRCSPPLGALVPVTAVCILCFVVGSGNVVTVMLIGRYDM 69
Db 6 AREGPGSAGWDLFP-----LFPAPLLAGVTATCVAFVAGVAGNLLTVLVVRREFL 57
QY 70 RTTNLYLGSMAYSDLLILGLPDLVRLWRSRPPWFGPPLLCLRLSLYVVGCTYATILHM 129
Db 58 RTTNLYLCSLACSDLLIFLCMPDLVRLWQYRPNWFGDILCKLFQFVSGCTYATVLT 117
QY 130 TALSVERYLAICRPLARVLVTRRRVRLATVAVALLSAGPPLFLVGVQDQPGISWVP 189
Db 118 TALSVERYFAICFPLRAKVLTKGRVKLALLAWAVAFCSAGPIFVLVGVHE----- 170
QY 190 GLNGTARIASSPLASPPPLMLSRAPPPSGPPTAAALFSRECRPS--PAQLGALRV 247
Db 171 --NGT-----DPRD-----TRECRATEFAVRSGLLTA 195
QY 248 MLWVTTAYFFLPCLSLYLIGLIGRELWSSRRPLRGPAASGRGRGHRGROTKRVLVVVLA 307
Db 196 MWVSVVFFLPVCLTVLYSLIGRLKLRGRGDTAGGASLRQSHRQTVKMLAVVVF 255
QY 308 ICWLPHVGRYIIVNTSDS---RMMYFSQYFNIVALQLFYLASINPILYNLSKKYRA 364
Db 256 IFCWLPHVGRYLFKSPFSGLEIAIQSYCNLVSFVLYLSAAINPILYNMSKKYRV 315
QY 365 AAFKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTETTSAN 407
Db 316 AVFKLLGFPFSSQKLSLTKDESR-----AWTESSIN 348
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RESULT 4
US-09-762-661A-7
; Sequence 7, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-762-661A-7
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Query Match 39.8%; Score 858.5; DB 4; Length 366;
Best Local Similarity 44.9%; Pred. No. 1.9e-65;
Matches 188; Conservative 55; Mismatches 105; Indels 71; Gaps 10;

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QY 57 VVTVMILGRVDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLMRSRPWFGPPLCRLSLY 116
Db 62 LLTMLVSVRFREMTTNNLYLSSMAFSDLLIFLCMLDPLFRLQYRPNWNLGNLLCKLPQF 121
QY 117 VGECTVATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLALVAVALLSAGPFLFL 176
Db 122 VSSECTVATLITLALSVERYFAICFPRLRAKVVTGKRVKLVILVIVAWAFCSAGPIFVL 181
QY 177 VGVQDQPGISVVPGLNGTARIASPLASPPMLSRAPPPSPGPTAEAAALFSRECR 236
Db 182 VGVHEHD-----NGT-----DPRD-----TNECR 199
QY 237 PS--PAQLGALRVMLWVTYAFYFPLFCILYGLIGRELWSSRRPLRGPAASG---RER 291
Db 200 ATFAVRSGLLTVMWVSSVFFPLFVCLTVLYSLIGRKLW---RRKRGAAVGSRLDQ 256
QY 292 GHRQTRKVLVAVLAFIICWLPFHVGRIIY---INTEDSRMMYFSQYFNIVALQLFYLSA 348
Db 257 NHQQTVMKLVAVVFAFICLWLPFHVGRIYFSKLEPGSVIEIAQISQYCNLVSVFLFYLSA 316
QY 349 SINPILYNLSKKYRAAFKILLARKSRPRGFRHSRDTAGEVAGDTGDTVGYTETSAN 407
Db 317 AINPILYNIMSKRYAVAVFKLGFEPFSQKSLTKDESSR-----AWTESSIN 365
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RESULT 5

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US-09-743-475-6
; Sequence 6, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Michael M.
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-743-475-6
```

Query Match 39.8%; Score 858.5; DB 4; Length 366;
Best Local Similarity 44.9%; Pred. No. 1.9e-65;
Matches 188; Conservative 55; Mismatches 105; Indels 71; Gaps 10;

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QY 5 WNGSDGEGA-----REPPWPALPPCD---ERRCSPPPLGALVPVAVCLCLFVVGSGN 56
Db 2 WNATPSEPGPNLTLPLDGLWDAPPENDSLVEELLPLFPPTLLAGVATCATCVAFVVGIA 61
QY 57 VVTVMILGRVDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLMRSRPWFGPPLCRLSLY 116
Db 62 LLTMLVSVRFREMTTNNLYLSSMAFSDLLIFLCMLDPLFRLQYRPNWNLGNLLCKLPQF 121
```

```
QY 117 VGECTVATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLALVAVALLSAGPFLFL 176
Db 122 VSSECTVATLITLALSVERYFAICFPRLRAKVVTGKRVKLVILVIVAWAFCSAGPIFVL 181
QY 177 VGVQDQPGISVVPGLNGTARIASPLASPPMLSRAPPPSPGPTAEAAALFSRECR 236
Db 182 VGVHEHD-----NGT-----DPRD-----TNECR 199
QY 237 PS--PAQLGALRVMLWVTYAFYFPLFCILYGLIGRELWSSRRPLRGPAASG---RER 291
Db 200 ATFAVRSGLLTVMWVSSVFFPLFVCLTVLYSLIGRKLW---RRKRGAAVGSRLDQ 256
QY 292 GHRQTRKVLVAVLAFIICWLPFHVGRIIY---INTEDSRMMYFSQYFNIVALQLFYLSA 348
Db 257 NHQQTVMKLVAVVFAFICLWLPFHVGRIYFSKLEPGSVIEIAQISQYCNLVSVFLFYLSA 316
QY 349 SINPILYNLSKKYRAAFKILLARKSRPRGFRHSRDTAGEVAGDTGDTVGYTETSAN 407
Db 317 AINPILYNIMSKRYAVAVFKLGFEPFSQKSLTKDESSR-----AWTESSIN 365
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RESULT 6

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US-09-077-675A-13
; Sequence 13, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-675A-13
```

Query Match 39.8%; Score 857.5; DB 3; Length 366;
Best Local Similarity 44.5%; Pred. No. 2.4e-65;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

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; LENGTH: 366 amino acids
; TYPE: amino acid
; Best alignment: 366 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-674-13

Query Match
Best Local Similarity 44.5%; Pred.No. 2.4e-65;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9

Qy 5 WNGSDQEGA-----REPPWALPPCD---ERRCSPPFLGALVPVTVAGVLCIFVVGVSQN 56
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 WNA TPSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCAVLPVVGIAQN 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 57 VVTVMILGRYDRMRTTNNLYLGSMAVSDLLILGLPFLDYLRWRSRPWFVGPILCRISLY 116
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 LLTMLVVSFRPRELRTNNLYLGSMAFSDLLIFLCMPDLVLRLWQYRPMWFGDILCKLQF 121
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 117 VGGGCTVATLLHWTALSVRYLAIQCPRLARVLVTRRRYLAIVLWALLSAGFFLEL 176
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 122 VSRSCTYAVLTTLALSVERYPFAICPPLRAKVVVTKGRVLVIFVIAWAFCSAGSIFVL 181
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 177 VGVQDPGISVWVGLNGTARIASSPLASPPFLWLSRAPPSPFSGPETAAAAALFSRRC 236
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 182 VGVHEH-----NGT-----DP-W-----DTEGR 199
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 237 PS--PAQLGNLRVLMVWTAYTFELPFLCLSLYGLIGRELNSRRPLRGPAAAGRGRHR 294
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 200 PTFEAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLWRRRRGDVAVVGASLRDQNHK 259
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 295 QTRKVLVVVLAFTICWLEPFHVGRIIYINTEDS---RMVYFSQYFNIVALQLFYLSASIN 351
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 260 QTVKMLAVVVEAFILCWLEFFHVGRIYLFKSPFGSLEIAQLISQYCNLVSFVLYLSAAIN 319
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 352 PLYNLISKKYRAAPKLLAKSRPRGRPHRSDRTAGEVAGDTGGDTGYTETSAN 407
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 320 PLYNIMSKRYAVFRLGFPFFSQRLSTLTKDSSR-----AWTESSIN 365
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 8
US-09-170-496D-88
; Sequence 88, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-C
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-88

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Query Match	39.8%;	Score	857.5;	DB 4;	Length	366;
Best Local Similarity	44.5%;	Pred. No.	2.4e-65;			
Matches	185;	Conservative	59;	Mismatches	107;	Indels
					65;	Gaps
					9;	

QY	5	WNGSDGPECA-----REPPWALPPCD---RRRCSPPLGALVPVTAVCLFVWGVS	56
	:	:	
Db	2	WNATSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVG	61
	:	:	
	:	:	
	:	:	
QY	57	VYVVMILIGRYDMRTTNLYLGSMAVSDLLILLGLPTDLYLWLSRPPWVFGLICRLSLY	116
	:	:	
	:	:	
	:	:	
Db	62	LUTLVMSRRELRRTTNLYLSSWAFSDLLIFLCMPDLVGLWLYRRPWNFGDLLCKLFQF	121
	:	:	
	:	:	
	:	:	
	:	:	

QY 117 VGECTYATLLHMTALSVERYLACRPLKARVLTERRRVALIAVLAVALLSAGPFLFL 176
Db 122 VSECTYATVLTALSVERYLACRPLKARVLTERRRVALIAVLAVALLSAGPFLFL 181
QY 177 VGEQDPGISVVPGLNGTARIASSPLAGSPPPLWLSRAPPPSPGPTAEAAALFSRECR 236
Db 182 VGEVHE-----NGT-----DP--W-----DTNECR 199
QY 237 PS--PAQIGALRVMLVWTAYFFFLCLSLIYGLIGRELWSSRRPLRGPAAASGRGHR 294
Db 200 PTEFAVRSGLLTVMVWSSIFFFLPVCLTVLYSLIGRKLWRRRRGDVAVGASLRDQNHK 259
QY 295 QTKRVLVVVLAFLICWLPFHVGRILYIINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
Db 260 QTVKMLAVVFAFILCWLPFHVGRILYIINTEDS---RMVFSQYFNIVALQLFYLSASIN 319
QY 352 PILYNLSKKYRAAFKULLARKSRPRGHRSDRTAGEVAGDTGDTVGYTETSAN 407
Db 320 PILYNIMSKYRVAVFRLLGFPFQSKLSTLKDESSR-----AWTESSIN 365

RESULT 9

US-09-743-742B-7

; Sequence 7, Application US/09743742B

; Patent No. 6599718

; GENERAL INFORMATION:

; APPLICANT: Howard, Andrew D.

; APPLICANT: McKee, Karen Kulju

; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED

; FILE REFERENCE: 20217P

; CURRENT APPLICATION NUMBER: US/09/743,742B

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: PCT/US99/15941

; PRIOR FILING DATE: 1999-07-13

; PRIOR FILING DATE: 1998-07-13

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 366

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-743-742B-7

Query Match 39.8%; Score 857.5; DB 4; Length 366;

Best Local Similarity 44.5%; Pred. No. 2.4e-65;

Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPCD---ERRCSPPLGALVPVTAACLCLFVVGVSGN 56
Db 2 WNAFSEEPGNLTADLDWDASFGNDSGLGDELQLQFPAPLAGVTATCVAFVVGAGN 61
QY 57 VVTVMILGRYDMRTTNLYLGSMAVSDLLILLGLPDLYLWRSRPVWFGPLLCRLSLY 116
Db 62 LLTMLVVSRRFELATTNLYLSSNAFSDLLIFLCMPDLVLWQVYRPNWFGDLCKLQF 121
QY 117 VGECTYATLLHMTALSVERYLACRPLKARVLTERRRVALIAVLAVALLSAGPFLFL 176
Db 122 VSECTYATVLTALSVERYLACRPLKARVLTERRRVALIAVLAVALLSAGPFLFL 181
QY 177 VGEQDPGISVVPGLNGTARIASSPLAGSPPPLWLSRAPPPSPGPTAEAAALFSRECR 236
Db 182 VGEVHE-----NGT-----DP--W-----DTNECR 199
QY 237 PS--PAQIGALRVMLVWTAYFFFLCLSLIYGLIGRELWSSRRPLRGPAAASGRGHR 294
Db 200 PTEFAVRSGLLTVMVWSSIFFFLPVCLTVLYSLIGRKLWRRRRGDVAVGASLRDQNHK 259
QY 295 QTKRVLVVVLAFLICWLPFHVGRILYIINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
Db 260 QTVKMLAVVFAFILCWLPFHVGRILYIINTEDS---RMVFSQYFNIVALQLFYLSASIN 319

QY 352 PILYNLSKKYRAAFKULLARKSRPRGHRSDRTAGEVAGDTGDTVGYTETSAN 407
Db 320 PILYNIMSKYRVAVFRLLGFPFQSKLSTLKDESSR-----AWTESSIN 365

RESULT 10

US-09-762-661A-5

; Sequence 5, Application US/09762661A

; Patent No. 6645726

; GENERAL INFORMATION:

; APPLICANT: Howard, Andrew D.

; APPLICANT: Palyha, Oksana C.

; APPLICANT: Smith, Roy G.

; APPLICANT: Tan, Carina P.

; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE

; FILE REFERENCE: 20207P

; CURRENT APPLICATION NUMBER: US/09/762,661A

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: PCT/US99/17915

; PRIOR FILING DATE: 1999-08-06

; PRIOR APPLICATION NUMBER: 60/095,960

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 366

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-762-661A-5

Query Match 39.8%; Score 857.5; DB 4; Length 366;

Best Local Similarity 44.5%; Pred. No. 2.4e-65;

Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPCD---ERRCSPPLGALVPVTAACLCLFVVGVSGN 56
Db 2 WNAFSEEPGNLTADLDWDASFGNDSGLGDELQLQFPAPLAGVTATCVAFVVGAGN 61
QY 57 VVTVMILGRYDMRTTNLYLGSMAVSDLLILLGLPDLYLWRSRPVWFGPLLCRLSLY 116
Db 62 LLTMLVVSRRFELATTNLYLSSNAFSDLLIFLCMPDLVLWQVYRPNWFGDLCKLQF 121
QY 117 VGECTYATLLHMTALSVERYLACRPLKARVLTERRRVALIAVLAVALLSAGPFLFL 176
Db 122 VSECTYATVLTALSVERYLACRPLKARVLTERRRVALIAVLAVALLSAGPFLFL 181
QY 177 VGEQDPGISVVPGLNGTARIASSPLAGSPPPLWLSRAPPPSPGPTAEAAALFSRECR 236
Db 182 VGEVHE-----NGT-----DP--W-----DTNECR 199
QY 237 PS--PAQIGALRVMLVWTAYFFFLCLSLIYGLIGRELWSSRRPLRGPAAASGRGHR 294
Db 200 PTEFAVRSGLLTVMVWSSIFFFLPVCLTVLYSLIGRKLWRRRRGDVAVGASLRDQNHK 259
QY 295 QTKRVLVVVLAFLICWLPFHVGRILYIINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
Db 260 QTVKMLAVVFAFILCWLPFHVGRILYIINTEDS---RMVFSQYFNIVALQLFYLSASIN 319
QY 352 PILYNLSKKYRAAFKULLARKSRPRGHRSDRTAGEVAGDTGDTVGYTETSAN 407
Db 320 PILYNIMSKYRVAVFRLLGFPFQSKLSTLKDESSR-----AWTESSIN 365

RESULT 11

US-09-364-425B-45

; Sequence 45, Application US/09364425B

; Patent No. 6653086

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.


```
; APPLICANT: Lin, I-Lin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Chen, Ruoping
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
; FILE REFERENCE: Azen0047
; CURRENT APPLICATION NUMBER: US/09/364,425B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/094,879
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/106,300
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/110,906
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 45
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-364-425B-45

Query Match      39.8%; Score 857.5; DB 4; Length 366;
Best Local Similarity 44.5%; Pred. No. 2.4e-65;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY      5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAVCICLFVVGSGN 56
Db      2 WNAATPSEPGFNLTADLDWDASFGNDSLGLDELQLFPAPLLAGVATATCVAFVVGIA 61

QY      57 VVTVMILGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYLWRSRPWVGPLLCRLSLY 116
Db      62 LLTMLVVSRRFRELTTNNLYLSSMAFSDLLIFLCMPDLVLWQYRPWNFGDLLCKLFQ 121

QY      117 VGECCYATLLHMTALSVRYLAICRPLRARVLVTRRRVRLALIAVLWAVALLSAGPELFL 176
Db      122 VSSECTATVLTITALSVERFYAICFPLRAKVVTGKRVKLVIFVIAVAFCSAGPIFVL 181

QY      177 VGYEQDGISVWPLNGTARIASSPLASSPPLWSRAPPPSPGPTAAALFSECR 236
Db      182 VGVHE-----NGT-----DP--W-----DTNECR 199

QY      237 PS--PAQLGALRMLVMTTAYFPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHR 294
Db      200 PTFEAVRSGLLTVMWVSSIFFLPVCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259

QY      295 QTKRVLLVVVLAFLICMLPHVGRRIIYNTEDS---RMVFSQYFNIVALQFLYLSASIN 351
Db      260 QTVKMLAVVVFALICMLPHVGRYLFSSKSFEPGSLIEIAQISQYCNLVSFVLYLSAIN 319

QY      352 PLYNLISKYRAAAPKLLARKSRPGRHRSRDTAGEVAGDTGGDTGVGTETSAN 407
Db      320 PLYNIMSKYRVAVFRLGFEPPFSQKSLTKDESSR-----AMTESSIN 365

RESULT 12
US-09-743-475-4
; Sequence 4, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
```

```
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-743-475-4

Query Match      39.8%; Score 857.5; DB 4; Length 366;
Best Local Similarity 44.5%; Pred. No. 2.4e-65;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY      5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAVCICLFVVGSGN 56
Db      2 WNAATPSEPGFNLTADLDWDASFGNDSLGLDELQLFPAPLLAGVATATCVAFVVGIA 61

QY      57 VVTVMILGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYLWRSRPWVGPLLCRLSLY 116
Db      62 LLTMLVVSRRFRELTTNNLYLSSMAFSDLLIFLCMPDLVLWQYRPWNFGDLLCKLFQ 121

QY      117 VGECCYATLLHMTALSVRYLAICRPLRARVLVTRRRVRLALIAVLWAVALLSAGPELFL 176
Db      122 VSSECTATVLTITALSVERFYAICFPLRAKVVTGKRVKLVIFVIAVAFCSAGPIFVL 181

QY      177 VGYEQDGISVWPLNGTARIASSPLASSPPLWSRAPPPSPGPTAAALFSECR 236
Db      182 VGVHE-----NGT-----DP--W-----DTNECR 199

QY      237 PS--PAQLGALRMLVMTTAYFPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHR 294
Db      200 PTFEAVRSGLLTVMWVSSIFFLPVCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259

QY      295 QTKRVLLVVVLAFLICMLPHVGRRIIYNTEDS---RMVFSQYFNIVALQFLYLSASIN 351
Db      260 QTVKMLAVVVFALICMLPHVGRYLFSSKSFEPGSLIEIAQISQYCNLVSFVLYLSAIN 319

QY      352 PLYNLISKYRAAAPKLLARKSRPGRHRSRDTAGEVAGDTGGDTGVGTETSAN 407
Db      320 PLYNIMSKYRVAVFRLGFEPPFSQKSLTKDESSR-----AMTESSIN 365

RESULT 13
US-09-077-675A-3
; Sequence 3, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-675A-3

Query Match          39.7%; Score 857; DB 3; Length 353;
Best Local Similarity 46.2%; Pred. No. 2,5e-65;
Matches 185; Conservative 53; Mismatches 96; Indels 66; Gaps 9;

QY 19 WPALPPCD---ERRCSPPFLGALVPTAVCLCLFVVGSGNVVTVMLIGRYDMMRTTNL 75
Db 8 WDAPPENDSLVEELLPLFPPTLLAGVTATCVALFVVGIAGNLLTMLVVSRRFEMRTTNL 67
QY 76 YLGSMVSDLLILLGLPDLVLRSPVWPGPLCRLSLYVGEGCTYATLLHMTALSVE 135
Db 68 YLSSMAFSDLLIFLCMLDLFRLMQYRPNLGNLCKLFQVSESTYATVLTITALSVE 127
QY 136 RYLAICRPLRARVLTTRRRVRLIAVLMAVALLSAGPFLFVGVQDPCGISVVPGLNGTA 195
Db 128 RYFALCFPLRAKVTVTKGRVILVILVAVAFCSAGPIFVLGVVHEH-----NGT- 177
QY 196 RIASSPLASSPPLMLSRAPPPSPGPGPETAAALFSSRCRPS--PAQIGALRVMLWVTT 253
Db 178 -----DPRD-----TNECRATEFAVRSGLLTVMVWVSS 205
QY 254 AVFFLPFLCLSTLYGLIGELWSSRRPLRGPAAG---RERCHROTQKRVLLVVLAFILC 310
Db 206 VFFFLPVFCLTVLYSLIGRKLW---RRKGEAAVSSLRDQNHQKTVKMLAVVVFALILC 262
QY 311 WLPFHVGRIIY---INTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAF 367
Db 263 WLPFHVGRLYFSKSLPGSVEIAQISQYCNLVSVFLVYLSAAILNIPILYNIMSKKYRVAVF 322
QY 368 KILLARKSRPRGFRHSRDTAGEVAGDTGGDTVGTYTETSAN 407
Db 323 KLLGPEPFSQKRLSTLKDESSR-----AWTESSIN 352

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RESULT 14

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US-09-077-674-3
; Sequence 3, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 B. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-674-3

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Best Local Similarity 46.2%; Pred. No. 2,5e-65;
Matches 185; Conservative 53; Mismatches 96; Indels 66; Gaps 9;

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Db 8 WDAPPENDSLVEELLPLFPPTLLAGVTATCVALFVVGIAGNLLTMLVVSRRFEMRTTNL 67
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Db 68 YLSSMAFSDLLIFLCMLDLFRLMQYRPNLGNLCKLFQVSESTYATVLTITALSVE 127
QY 136 RYLAICRPLRARVLTTRRRVRLIAVLMAVALLSAGPFLFVGVQDPCGISVVPGLNGTA 195
Db 128 RYFALCFPLRAKVTVTKGRVILVILVAVAFCSAGPIFVLGVVHEH-----NGT- 177
QY 196 RIASSPLASSPPLMLSRAPPPSPGPGPETAAALFSSRCRPS--PAQIGALRVMLWVTT 253
Db 178 -----DPRD-----TNECRATEFAVRSGLLTVMVWVSS 205
QY 254 AVFFLPFLCLSTLYGLIGELWSSRRPLRGPAAG---RERCHROTQKRVLLVVLAFILC 310
Db 206 VFFFLPVFCLTVLYSLIGRKLW---RRKGEAAVSSLRDQNHQKTVKMLAVVVFALILC 262
QY 311 WLPFHVGRIIY---INTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAF 367
Db 263 WLPFHVGRLYFSKSLPGSVEIAQISQYCNLVSVFLVYLSAAILNIPILYNIMSKKYRVAVF 322
QY 368 KILLARKSRPRGFRHSRDTAGEVAGDTGGDTVGTYTETSAN 407
Db 323 KLLGPEPFSQKRLSTLKDESSR-----AWTESSIN 352

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RESULT 15

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US-09-077-675A-16
; Sequence 16, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY

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; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-675A-16

Query Match 39.7%; Score 855.5; DB 3; Length 364;
Best Local Similarity 48.0%; Pred. No. 3.5e-65;
Matches 184; Conservative 52; Mismatches 82; Indels 65; Gaps 11;

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2 WNAT--PSEEPNPVTLDDWDASPGNDSLDPDLLPLFPAPLLAGVATCATCVAFVVGISG 59
QY 56 NVVTVMILIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLCLRLSL 115
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60 NLTLMLVVSFRFURTTNLYLSSMAFSDDLIFLCNPLDLVRLWQYRPWNFGDLCCKLFQ 119
QY 116 YVGGCTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLF 175
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120 FVSESCYATVLTITALSVERYFAICFPFLRAKVVTGKRVKLVILVIWAVAFCSAGPIFV 179
QY 176 LVGVEQDPGISVVPGLNGTARIASSPLASPLWLSRAPPPSPSGPETAAALFSREC 235
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
180 LVGVEHE-----NGT-----DPRD-----TNEC 197
QY 236 RPS--PAQLGALVMLWVTYATYFELPFLCLILYGLIGRELWSSRRPLRGPAASG---RE 290
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
198 RATEFAVRSGLLTVWVWSSVFFFLPVFCLTVLYSLIGRKLW--RR--RGDAAVGASLRD 253
QY 291 RGHQRTKRVLLVVVLAFLICMLPFGVGRRIIYNTEDS---RMMYFSQYFNIVALQLFYLS 347
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
254 QNHKQTVKMLAVVVFAPFLCWLPHVGRYLFPSKFGPSLEIAQISQYCNLVSPVLYLS 313
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Search completed: July 4, 2004, 03:11:25
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 03:11:28 ; Search time 78 Seconds
(without alignments)
1644.217 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPWNGSDGEGAREPWPDTGGDTVGTTTSANVKTMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2156	100.0	412	12	US-09-876-252-130
2	2156	100.0	412	15	US-10-417-820A-130
3	2156	100.0	412	15	US-10-417-820A-150
4	2156	100.0	412	16	US-10-723-955-130
5	2149	99.7	412	14	US-10-225-567A-473
6	2149	99.7	412	14	US-10-290-078-15
7	2149	99.7	412	14	US-10-318-661-28
8	2149	99.7	412	14	US-10-206-677-2
9	864.5	40.1	366	14	US-10-251-385-210
10	857.5	39.8	366	14	US-10-251-385-88
11	857.5	39.8	366	14	US-10-303-204A-13
12	857.5	39.7	353	14	US-10-303-204A-3
13	855.5	39.7	364	14	US-10-303-204A-16
14	854	39.6	361	14	US-10-303-204A-8
15	769.5	35.7	302	14	US-10-303-204A-2

16	768.5	35.6	302	14	US-10-303-204A-7
17	668.5	31.0	271	14	US-10-303-204A-12
18	638.5	29.6	289	14	US-10-225-567A-140
19	638.5	29.6	289	14	US-10-303-204A-10
20	627	29.1	289	14	US-10-303-204A-5
21	498	23.1	418	11	US-09-826-509-535
22	491	22.8	418	14	US-10-225-567A-207
23	490.5	22.8	403	14	US-10-251-385-224
24	485.5	22.5	445	15	US-10-240-145-53
25	485.5	22.5	445	15	US-10-240-145-139
26	484.5	22.5	403	14	US-10-251-385-114
27	484.5	22.5	403	14	US-10-225-567A-540
28	484.5	22.5	403	14	US-10-290-078-18
29	484.5	22.5	403	15	US-10-353-690-10
30	474	22.0	402	12	US-10-258-423-4
31	474	22.0	412	14	US-10-225-567A-557
32	474	22.0	415	12	US-09-875-076-12
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34	474	22.0	415	12	US-10-258-423-2
35	474	22.0	415	14	US-10-272-883-12
36	474	22.0	415	14	US-10-393-807-12
37	474	22.0	415	15	US-10-417-820A-12
38	474	22.0	415	16	US-10-723-955-12
39	472.5	21.9	395	12	US-10-258-423-6
40	472.5	21.9	396	12	US-10-258-423-8
41	467.5	21.7	426	12	US-10-311-671-1
42	434	20.1	418	15	US-10-369-493-5319
43	430	19.9	419	9	US-09-804-551B-26
44	430	19.9	428	14	US-10-270-333-114
45	414	19.2	410	11	US-09-826-509-537

ALIGNMENTS

RESULT 1

US-09-876-252-130
; Sequence 130, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Rec
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946

; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 130
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-130

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Best Local Similarity 100.0%; Pred. No. 1.7e-168;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 MLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGFLCLRLSLYVGE 120
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Db 121 CTYATLLHMTALSVERYIAICRPIRARVLTTRRRVRLIAVLWAVALLSAGPFLVGV 180
Qy 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPSPSPETAEEAALFSRECRSPA 240
Db 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPSPSPETAEEAALFSRECRSPA 240
Qy 241 QLGALRWMLVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTKRVL 300
Db 241 QLGALRWMLVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTKRVL 300
Qy 301 LVVLAFLICWLPFHVGRRIIYNTEDSRMMYFSQYFNIVALQLFYLASINPILYNLSK 360

Db 301 LVVLAFLICWLPFHVGRRIIYNTEDSRMMYFSQYFNIVALQLFYLASINPILYNLSK 360
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Db 361 KYRAAFAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGTYTETSANVKTMG 412
RESULT 2
US-10-417-820A-130
; Sequence 130, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 130
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-820A-130

Query Match 100.0%; Score 2156; DB 15; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.7e-168;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGSPWNGSDGEGAREPPWALPCDERRCSPFLGALVPTAVCLCLFVVGVSGNVVTV 60
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Db 61 MLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGFLCLRLSLYVGE 120
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Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
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RESULT 3
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; Sequence 150, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 150
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-820A-150

Query Match 100.0%; Score 2156; DB 15; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.7e-168;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSFPFLGALVPVTAVALCLFVVGSGNVTV 60
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSFPFLGALVPVTAVALCLFVVGSGNVTV 60

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Db 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLCLSLYVGE 120

Qy 121 CYYATLLHMTALSVERYLAI CRLRVLVTRRRVALLI AVALLSAGPFLVGV 180
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Qy 181 QDPGIVVPGINGTARIASSPPLWLSRAPPSPSPETAATAAALFSRECRPSA 240

Db 181 QDPGIVVPGINGTARIASSPPLWLSRAPPSPSPETAATAAALFSRECRPSA 240
Qy 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTKRVL 300
Db 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTKRVL 300
Qy 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Qy 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGVTETTSANVKTWG 412
Db 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGVTETTSANVKTWG 412

RESULT 4
US-10-723-955-130
; Sequence 130, Application US/10723955
; Publication No. US20040110238A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehman-Bruinsma, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huang T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin
; APPLICANT: White, Carol
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US29.CON
; CURRENT APPLICATION NUMBER: US/10/723,955
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 10/417,820
; PRIOR FILING DATE: 2003-4-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-955-130

Query Match 100.0%; Score 2156; DB 16; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.7e-168;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSFPFLGALVPVTAVALCLFVVGSGNVTV 60
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSFPFLGALVPVTAVALCLFVVGSGNVTV 60

Qy 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLCLSLYVGE 120

Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYLWRSRPWFPGCLCRSLVVGEG 120
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSECRPSPA 240
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSECRPSPA 240
QY 241 QLGALRVMLVWTTAYFFLPCLCSILYGLIGRELWSSRRPLRGPAAASGRERGHQTRVRL 300
Db 241 QLGALRVMLVWTTAYFFLPCLCSILYGLIGRELWSSRRPLRGPAAASGRERGHQTRVRL 300
QY 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
QY 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412
Db 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412
RESULT 5
US-10-225-567A-473
; Sequence 473, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 473
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-473
Query Match 99.7%; Score 2149; DB 14; Length 412;
Best Local Similarity 99.8%; Pred. No. 6.3e-168;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPEGAREPPWLPALPCDERRCSPPLGALVPVTAVCLCLFVVGSGNVTV 60
Db 1 MGSPWNGSDGPEGAREPPWLPALPCDERRCSPPLGALVPVTAVCLCLFVVGSGNVTV 60
QY 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYLWRSRPWFPGCLCRSLVVGEG 120
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYLWRSRPWFPGCLCRSLVVGEG 120
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSECRPSPA 240
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSECRPSPA 240
QY 241 QLGALRVMLVWTTAYFFLPCLCSILYGLIGRELWSSRRPLRGPAAASGRERGHQTRVRL 300
Db 241 QLGALRVMLVWTTAYFFLPCLCSILYGLIGRELWSSRRPLRGPAAASGRERGHQTRVRL 300
QY 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360

Db 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
QY 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412
Db 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412
RESULT 6
US-10-290-078-15
; Sequence 15, Application US/102900078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692 or 58874
; FILE REFERENCE: MPI2001-288P1(W)
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-078-15
Query Match 99.7%; Score 2149; DB 14; Length 412;
Best Local Similarity 99.8%; Pred. No. 6.3e-168;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPEGAREPPWLPALPCDERRCSPPLGALVPVTAVCLCLFVVGSGNVTV 60
Db 1 MGSPWNGSDGPEGAREPPWLPALPCDERRCSPPLGALVPVTAVCLCLFVVGSGNVTV 60
QY 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYLWRSRPWFPGCLCRSLVVGEG 120
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYLWRSRPWFPGCLCRSLVVGEG 120
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSECRPSPA 240
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSECRPSPA 240
QY 241 QLGALRVMLVWTTAYFFLPCLCSILYGLIGRELWSSRRPLRGPAAASGRERGHQTRVRL 300
Db 241 QLGALRVMLVWTTAYFFLPCLCSILYGLIGRELWSSRRPLRGPAAASGRERGHQTRVRL 300
QY 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
QY 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412
Db 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412
RESULT 7
US-10-318-661-28
; Sequence 28, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; FILE REFERENCE: UCAL-049C1P2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446

; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-661-28

Query Match 99.7%; Score 2149; DB 14; Length 412;
Best Local Similarity 99.8%; Pred. No. 6.3e-168;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVALCLCLFVVGSGNVTV 60
DB 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVALCLCLFVVGSGNVTV 60
QY 61 MLIORYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPGLLCRLSLYVGE 120
DB 61 MLIORYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPGLLCRLSLYVGE 120
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180
DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
QY 241 QLGALRVMLWTTTAYFFLPFLCISLYLIGRELWSSRRPLRGPAASGRERHROTQVRL 300
DB 241 QLGALRVMLWTTTAYFFLPFLCISLYLIGRELWSSRRPLRGPAASGRERHROTQVRL 300
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQVFNIVALQFLYLSASINPILYNLISK 360
DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQVFNIVALQFLYLSASINPILYNLISK 360
QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTSTANVKTWG 412
DB 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTSTANVKTWG 412

RESULT 8

US-10-206-677-2
; Sequence 2, Application US/10206677
; Publication No. US20030186336A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences, Inc.
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; APPLICANT: Kullander, Bruce G.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO
; FILE REFERENCE: 1920-1-8
; CURRENT APPLICATION NUMBER: US/10/206,677
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/250,251
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,452
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-206-677-2

Query Match 99.7%; Score 2149; DB 14; Length 412;
Best Local Similarity 99.8%; Pred. No. 6.3e-168;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVALCLCLFVVGSGNVTV 60
DB 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVALCLCLFVVGSGNVTV 60
QY 61 MLIORYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPGLLCRLSLYVGE 120
DB 61 MLIORYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPGLLCRLSLYVGE 120
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180
DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
QY 241 QLGALRVMLWTTTAYFFLPFLCISLYLIGRELWSSRRPLRGPAASGRERHROTQVRL 300
DB 241 QLGALRVMLWTTTAYFFLPFLCISLYLIGRELWSSRRPLRGPAASGRERHROTQVRL 300
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQVFNIVALQFLYLSASINPILYNLISK 360
DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQVFNIVALQFLYLSASINPILYNLISK 360
QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTSTANVKTWG 412
DB 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTSTANVKTWG 412

RESULT 9

US-10-251-385-210
; Sequence 210, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 210
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-210

Query Match 40.1%; Score 864.5; DB 14; Length 366;
Best Local Similarity 44.7%; Pred. No. 1.3e-62;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----RBPWPALPPCD---ERRCSPFLGALVPVTAVALCLCLFVVGSGN 56
DB 2 WNATPSEEPGNLTADLDWDASFGNDSLGLDELLQLFPAPLAGVATCTVALFVVGIAKN 61
QY 57 VVTWNLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPGLLCRLSLY 116
DB 62 LLTLMVSRFRRLTNNLYLSSMAFSDLLIFLCWPLDLVRLWQVYRPNWFGDLCKLQF 121
QY 117 VGECTATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFL 176
DB 122 VSECTATVLTITALSVERYLAICFLRAKVVVTKGRKLVIFVIAVAFCSAGPIVL 181


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QY 177 VGEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
Db 182 VGEHE-----NGT-----DP--W-----DINECR 199
QY 237 PS--PAQGLARVLMVWTTAYFFLPCLSLYGLIGRELMSSRRPLRGPAAASGRGRHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY 295 QTKRVLVVVLAFLICWLPFHVGRILYINTEDS---RMVFSQYFNIVALQFLYLSASIN 351
Db 260 QTKMGLAVVVFAPILCWLPFHVGRILYINTEDS---RMVFSQYFNIVALQFLYLSASIN 319
QY 352 PILYNLSKKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGTVGYTETSAN 407
Db 320 PILYNMSKKYRAVAVFLLGFEPFSQKSLTLKDESSR-----AWTESSIN 365

RESULT 10
US-10-251-385-88
; Sequence 88, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 88
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-88

Query Match 39.8%; Score 857.5; DB 14; Length 366;
Best Local Similarity 44.5%; Pred. No. 4.8e-62;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPPLGALVPVTAVCLCLFVVGSGN 56
Db 2 WNATPSEEPGNLTADLDWDASPGNDSLGLDQLLPAPLLAGVTATCVAFVVGIGN 61
QY 57 VVTVMILIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLY 116
Db 62 LTLMLVVSFRRLRTTNNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQF 121
QY 117 VGEQCTATLLHMTALSVRYLAICRPLARVLVTRRRVRLTAVLWALLSAGPFLFL 176
Db 122 VSESCYATVLTITALSVERYPFAICPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFVL 181
QY 177 VGEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
Db 182 VGEHE-----NGT-----DP--W-----DINECR 199
QY 237 PS--PAQGLARVLMVWTTAYFFLPCLSLYGLIGRELMSSRRPLRGPAAASGRGRHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY 295 QTKRVLVVVLAFLICWLPFHVGRILYINTEDS---RMVFSQYFNIVALQFLYLSASIN 351
Db 260 QTKMGLAVVVFAPILCWLPFHVGRILYINTEDS---RMVFSQYFNIVALQFLYLSASIN 319
QY 352 PILYNLSKKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGTVGYTETSAN 407
Db 320 PILYNMSKKYRAVAVFLLGFEPFSQKSLTLKDESSR-----AWTESSIN 365

RESULT 12
US-10-303-204A-13
; Sequence 13, Application US/10303204A
; Publication No. US20030106144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris E.
; APPLICANT: Feigener, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; TITLE OF INVENTION: FAMILY
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR FILING DATE: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR FILING DATE: 1996-12-10
; PRIOR FILING DATE: 1996-018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 366
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-303-204A-13

Query Match 39.8%; Score 857.5; DB 14; Length 366;
Best Local Similarity 44.5%; Pred. No. 4.8e-62;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPPLGALVPVTAVCLCLFVVGSGN 56
Db 2 WNATPSEEPGNLTADLDWDASPGNDSLGLDQLLPAPLLAGVTATCVAFVVGIGN 61
QY 57 VVTVMILIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLY 116
Db 62 LTLMLVVSFRRLRTTNNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQF 121
QY 117 VGEQCTATLLHMTALSVRYLAICRPLARVLVTRRRVRLTAVLWALLSAGPFLFL 176
Db 122 VSESCYATVLTITALSVERYPFAICPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFVL 181
QY 177 VGEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
Db 182 VGEHE-----NGT-----DP--W-----DINECR 199
QY 237 PS--PAQGLARVLMVWTTAYFFLPCLSLYGLIGRELMSSRRPLRGPAAASGRGRHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY 295 QTKRVLVVVLAFLICWLPFHVGRILYINTEDS---RMVFSQYFNIVALQFLYLSASIN 351
Db 260 QTKMGLAVVVFAPILCWLPFHVGRILYINTEDS---RMVFSQYFNIVALQFLYLSASIN 319
QY 352 PILYNLSKKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGTVGYTETSAN 407
Db 320 PILYNMSKKYRAVAVFLLGFEPFSQKSLTLKDESSR-----AWTESSIN 365
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RESULT 11
US-10-303-204A-13
; Sequence 13, Application US/10303204A
; Publication No. US20030106144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris E.
; APPLICANT: Feigener, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; TITLE OF INVENTION: FAMILY
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR FILING DATE: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR FILING DATE: 1996-12-10
; PRIOR FILING DATE: 1996-018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 366
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-303-204A-13
```

```
Query Match 39.8%; Score 857.5; DB 14; Length 366;
Best Local Similarity 44.5%; Pred. No. 4.8e-62;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPPLGALVPVTAVCLCLFVVGSGN 56
Db 2 WNATPSEEPGNLTADLDWDASPGNDSLGLDQLLPAPLLAGVTATCVAFVVGIGN 61
QY 57 VVTVMILIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLY 116
Db 62 LTLMLVVSFRRLRTTNNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQF 121
QY 117 VGEQCTATLLHMTALSVRYLAICRPLARVLVTRRRVRLTAVLWALLSAGPFLFL 176
Db 122 VSESCYATVLTITALSVERYPFAICPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFVL 181
QY 177 VGEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
Db 182 VGEHE-----NGT-----DP--W-----DINECR 199
QY 237 PS--PAQGLARVLMVWTTAYFFLPCLSLYGLIGRELMSSRRPLRGPAAASGRGRHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY 295 QTKRVLVVVLAFLICWLPFHVGRILYINTEDS---RMVFSQYFNIVALQFLYLSASIN 351
Db 260 QTKMGLAVVVFAPILCWLPFHVGRILYINTEDS---RMVFSQYFNIVALQFLYLSASIN 319
QY 352 PILYNLSKKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGTVGYTETSAN 407
Db 320 PILYNMSKKYRAVAVFLLGFEPFSQKSLTLKDESSR-----AWTESSIN 365

RESULT 12
US-10-303-204A-13
; Sequence 3, Application US/10303204A
; Publication No. US20030106144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
```

```

; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; TITLE OF INVENTION: FAMILY
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-3

```

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Query Match      39.7%; Score 857; DB 14; Length 353;
Best Local Similarity 46.2%; Pred. No. 5,1e-62;
Matches 185; Conservative 53; Mismatches 96; Indels 66; Gaps 9;

QY 19 WPALPPCD---ERRCSPPPLGALVPVTAVALCLFVVGSGNVVTVMLIGRYRDMETTNL 75
DB 8 WDAPPENDSLVEELPLPPTPLAGVTATCTVALFVVGAGNLLTMLVVSFRFEMTTNL 67
QY 76 YLGSMASDILLILGLPDLXLMRSRPPWFGPCLLCRLSLXYGEGCTYATLHMTALSV 135
DB 68 YLSSMAFSDDLIFLCMPDLDFRLMQYRPNWNLGKLFQFVSECTYATVLTITALSVE 127
QY 136 RYLAICRPLRVLVTRRRVRLAIVLWALLSAGPFLFVGVQDPGISVVPGLNGTA 195
DB 128 RYFAICFPLRAKVVVTKGRVKLVILVWAVAFCSAGPIFVLGVGVDH-----NGT- 177
QY 196 RIASSPLASSPPLWLSRAPPPSPGPGTAAALFSPRECPS---PAOLGALRVMLWTT 253
DB 178 -----DPRD-----TNECRATEFAVRSGLLTVMWVSS 205
QY 254 AYFELPFLCLILYGLIGRELWSSRRPLRGPAAG---RERGHQTKRVLVVLVLAFLIC 310
DB 206 VFFELPVFLVLYSLIGRKLW---RRKRGEAAVGSLLRDQNHQTVKMLAVVVFALIC 262
QY 311 WLPFHVGRIIY---INTEDSRMYFSQYFNIVALOLFYLASINPILYNILSKKYRAAF 367
DB 263 WLPFHVGRIYFSKSLPQSGVIAQISQYCNLVFSVFLYLSAIPILYNILSKKYRVAVF 322
QY 368 KILLARKSRPGRGHRSDTAGEVAGDTGGDTVGYTETSAN 407
DB 323 KLLGPEPSQKSLTKLDESSR-----AWTESSIN 352

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RESULT 13
US-10-303-204A-16
; Sequence 16, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR

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; TITLE OF INVENTION: FAMILY
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 364
; TYPE: PRT
; ORGANISM: rattus norvegicus
US-10-303-204A-16

Query Match      39.7%; Score 855.5; DB 14; Length 364;
Best Local Similarity 48.0%; Pred. No. 7e-62;
Matches 184; Conservative 52; Mismatches 82; Indels 65; Gaps 11;

QY 5 WNGSDGREGAREP-----PWPALPPCD---ERRCSPPPLGALVPVTAVALCLFVVGSG 55
DB 2 WNAT--PSEEPENVTLDLDWDASPGNDSLDELPLFPAPLLAGVTATCTVALFVVGISG 59
QY 56 NVVTVMLIGRYRDMETTNLYLGSMASVSDLLILGLPDLXLMRSRPPWFGPCLLCRLSL 115
DB 60 NLLTMLVVSFRFEMTTTNLYLSSMAFSDDLIFLCMPDLDFRLMQYRPNWNLGKLFQ 119
QY 116 YVGSGCTYATLHMTALSVRYLAICRPLRVLVTRRRVRLAIVLWALLSAGPFLF 175
DB 120 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVILVWAVAFCSAGPIFV 179
QY 176 LVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSPREC 235
DB 180 LVGVEH-----NGT-----DPRD-----TNEC 197
QY 236 RPS---PAOLGALRVMLWTTAYFELPFLCLILYGLIGRELWSSRRPLRGPAAG---RE 290
DB 198 RATEFAVRSGLLTVMWVSSVFFELPVFLVLYSLIGRKLW---RR--RGDAVAGSLRD 253
QY 291 RGHQTKRVLVVLVLAFLICWLPFHVGRIIYINTEDS---RMYFSQYFNIVALOLFYL 347
DB 254 QNHQTVKMLAVVVFALICWLPFHVGRIYFSKSLPQSGVIAQISQYCNLVFSVFLYLS 313
QY 348 ASINPILYNILSKKYRAAFKLL 370
DB 314 AAINPILYNILSKKYRVAVFKLL 336

RESULT 14
US-10-303-204A-8
; Sequence 8, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445

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; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-303-204A-8

Query Match 39.6%; Score 854; DB 14; Length 361;
Best Local Similarity 45.8%; Pred. No. 9,1e-62;
Matches 182; Conservative 57; Mismatches 98; Indels 60; Gaps 8;

QY 19 WPAIPCCD---ERRCSPFPLGALVPTAVCLCLFVVGSGNVVTVMLIGRYDMRTTNL 75
Db 16 WDA SPGNDLSIGDELLQLFPAPLLAGVTATCVAFVVGIAGNLLTMLVSRFRELRTTNL 75
QY 76 YLGSMVSDLLILGLGPFDLVLRSPVVRGPELLCLSLYVCEGCTYATLHMTALSVE 135
Db 76 YLSSWAFSDLLIFLCMLDLRLWQTRPNFGDLCKLQFQVSECTYATVITITALSVE 135
QY 136 RYLAICRPLRARVLTTRRRVRLAIYLVAVALLSAGPFLVLVGEQDPGISVVPGLNGTA 195
Db 136 RYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVLVGEHE-----NGT- 185
QY 196 RIASSPLASSPPLWLSRAPPPSPGPETAARAAALFSRECRPS--PAQIGALRVMLWVT 253
Db 186 -----DP--W-----DTNECRPTFAVRSGLLTVMVVWSS 213
QY 254 AYFFLPFLCLSLIYGLIGRELWSSRRPLRGPAASGRGHRGROTQKRVLLVWLAFICWLP 313
Db 214 IFFFLPVFCLTVLYSLIGRLKRRRGDAVGSASLDQNHKQTVKMLAVVVFILCWLP 273
QY 314 FHVGRIIYINTEDS-----RMVYSQYFNIVALQFYLSASINPILYNLSKRYRAAFKLL 370
Db 274 FHVGRIYFSKSPFGSLGSLAQISQYCNLVSVFLVYLSAAINPILYNLSKRYRAAFKLL 333
QY 371 LARKSRPRGFRHSRDTAGEVAGTGGDTGYTETSAN 407
Db 334 GPFPFSQKSLTLKDESSR-----AWTESSIN 360

RESULT 15

US-10-303-204A-2
; Sequence 2, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; TITLE OF INVENTION: FAMILY
; FILE REFERENCE: 19589PCN
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2
; LENGTH: 302
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-2

Query Match 35.7%; Score 769.5; DB 14; Length 302;
Best Local Similarity 46.3%; Pred. No. 6,3e-55;
Matches 165; Conservative 48; Mismatches 80; Indels 63; Gaps 8;

QY 60 VMLIGRYDMRTTNLYLGSMVSDLLILGLGPFDLVLRSPVVRGPELLCLSLYVCE 119
Db 1 MLVSRFREMRTTNLYLSSWAFSDLLIFLCMLDLRLWQTRPNFGDLCKLQFQVSE 60
QY 120 GCTYATLHMTALSVERVLAICRPLRARVLTTRRRVRLAIYLVAVALLSAGPFLV 179
Db 61 SCTYATVITITALSVERVFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIF 120
QY 180 EQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAARAAALFSRECRPS- 238
Db 121 EHD-----NGT-----DPRD-----TNECRATE 138
QY 239 -PAQIGALRVMLWVTYATFFLPFLCLSLIYGLIGRELWSSRRPLRGPAASG---BERGHR 294
Db 139 FAVRSGLLTVMVWSSVFFFLPVFCLTVLYSLIGRKLW---RRKRGAAVGSASLDQNHK 195
QY 295 QPKRVLLVVLAFILCWLPPEHVGRITII---INTEDSRMMYFSQYFNIVALQFYLSASIN 351
Db 196 QTVKMLAVVVFILCWLPPEHVGRILFSLKSPGSGVEIAQISQYCNLVSVFLVYLSA 255
QY 352 PILYNLSKRYRAAFKLLLARKSRPRGFRHSRDTAGEVAGTGGDTGYTETSAN 407
Db 256 PILYNLSKRYRAVAVFKLLGPFPFSQKSLTLKDESSR-----AWTESSIN 301

Search completed: July 4, 2004, 03:16:30
JOB time : 79 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 03:07:32 ; Search time 28 Seconds
(without alignments)
1415.390 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPWNGSDGPGAREPPWP.....DTGGDTVGTYTSANVKTMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	23.1	424	2 JH0164	neurotensin recept
2	491	22.8	418	2 S29506	neurotensin recept
3	451	20.9	477	2 JC7913	capa receptor (Cgl
4	434	20.1	418	2 A88013	Protein K10B4.4 [1
5	401	18.6	416	2 S68822	neurotensin recept
6	378	17.5	378	2 T15816	hypothetical prote
7	358	16.6	363	2 I57940	somatostatin recep
8	356.5	16.5	418	2 A46226	somatostatin recep
9	343	15.9	363	2 I57955	somatostatin recep
10	343	15.9	364	2 JN0763	somatostatin recep
11	342.5	15.9	380	2 AS5259	kappa opioid recep
12	338	15.7	352	2 JE0296	thyrotropin releas
13	338	15.7	380	2 S36143	kappa opioid recep
14	334	15.5	380	2 JC2338	kappa opioid recep
15	334	15.5	388	2 JN0605	somatostatin recep
16	333.5	15.5	367	2 I49022	kappa opioid recep
17	333.5	15.5	367	2 JC2421	opioid receptor ho
18	333.5	15.5	367	2 I56520	G protein-coupled
19	333.5	15.5	428	2 S30508	probable G protein
20	330.5	15.3	428	2 A44021	somatostatin recep
21	329.5	15.3	370	2 S43087	orphan opioid rece
22	328	15.2	380	2 A48227	kappa opioid recep
23	327	15.2	380	2 JC2434	kappa opioid recep
24	326.5	15.1	384	2 A47249	brain-specific som
25	325.5	15.1	372	2 I38532	delta opioid recep
26	321	14.9	384	2 JC4629	somatostatin recep
27	320.5	14.9	372	2 S34592	delta opioid recep
28	320.5	14.9	398	2 JN0708	thyrotropin-releas
29	320	14.8	519	2 S17783	tachykinin recepto

30	319	14.8	372	2 B48227	delta opioid recep
31	318.5	14.8	387	2 JC5949	galanin receptor 2
32	318	14.7	380	2 I38435	angiotensin recept
33	317	14.7	398	1 JQ1059	neurokinin 2 recep
34	317	14.7	411	2 I56444	thyrotropin-relea
35	317	14.7	412	2 S23436	thyroliberin recep
36	316	14.7	393	2 A39251	thyrotropin-releas
37	314	14.6	391	2 C41795	somatostatin recep
38	311	14.4	373	2 JE0087	delta opioid recep
39	311	14.4	384	1 S00516	neurokinin 2 recep
40	310	14.4	391	2 A39297	somatostatin recep
41	308.5	14.3	369	2 D41795	somatostatin recep
42	308.5	14.3	392	2 S65693	opioid receptor mu
43	308.5	14.3	400	2 I56553	mu opiate receptor
44	308	14.3	391	2 A41795	somatostatin recep
45	308	14.3	398	2 I56517	mu opioid receptor

ALIGNMENTS

RESULT 1

JH0164

neurotensin receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 17-Mar-2000

C:Accession: JH0164

R:Tanaka, K.; Masu, M.; Nakanishi, S.

Neuron 4, 847-854, 1990

A:Title: Structure and functional expression of the cloned rat neurotensin receptor.

A:Reference number: JH0164; MUID:90297956; PMID:1694443

A:Accession: JH0164

A:Molecule type: mRNA

A:Residues: 1-424 <TAN>

C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. This receptor (neurotensin) in the brain and as a hormone) cellular mediator in peripheral tissue

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

F:65-87/Domain: transmembrane #status predicted <TM1>

F:97-121/Domain: transmembrane #status predicted <TM2>

F:144-165/Domain: transmembrane #status predicted <TM3>

F:189-210/Domain: transmembrane #status predicted <TM4>

F:236-260/Domain: transmembrane #status predicted <TM5>

F:309-330/Domain: transmembrane #status predicted <TM6>

F:348-372/Domain: transmembrane #status predicted <TM7>

F:4,38,42/Binding site: carbohydrate (Asn) #status predicted

Query Match

Best Local Similarity 23.1%; Score 498; DB 2; Length 424;

Matches 125; Conservative 58; Mismatches 11; Indels 86; Gaps 11;

QY 39 PVPTAVCLCLFVGVSGNVVTVMILGR---YRDMETTNLYLGSMVSDLLI-LIGLPED 94

Db 65 VLVTATYALFVGVGVGNSVTAFTLARKKSLQSLQSTVHYHLGSLALSDLLILLAMPVE 124

QY 95 LYR-LWRGRPVVFGPLCLSLYGVGEGCTYATLHMTALSVERYLAIQCPURARVIVTER 153

Db 125 LYNFTWVHPWAFGADGCGYFFLRDACTYATLVNVALSVERYLAIQHPFKAKTINRS 184

QY 154 RVRALIAVLNAVALISAGFFFLVGVGQDPGISVVPGLNGTARIASSPLASSPPLWLSRA 213

Db 185 RTKKFISALWLASALLAIPMLFTWGLQNSGDGTHFG-----GLVCTIVT----- 231

QY 214 PPPSPSPGETAAEAALFSRECRPSPAOLGALRVMLWTTAYFFL-PFLCISILYGLIGR 272

Db 232 -----ATVKVVIQVNTFMSFLFPMVLVI-SILNTVIAN 262

QY 273 ELWSSRRRLRGPAAAGR-----EEGHRQTKR-----VLLVVLVLAII 309

Db 263 KLTVM---VHQAAQGRVCTVGTGTHNGLEHSTFNMTIEPRVQALRHGVLRVAVIAFW 319

QY 310 CWLPFPHVGRITTYINTEDSR---MMYFSQYFNIVALQFLYSASINPTLYNLISKYRAA 365

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Db 320 CWLPYHVRRLMFCYISDEQWTFLEDFYHYFYLMTNALFVSSAINPILNLYSANPRQV 379
QY 366 AFKLLLA-----RKSRP 377
Db 380 FLSTLACLCPGWRHRRKKRP 399

RESULT 2
S29506
neurotensin receptor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C;Accession: S29506
P;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kachad, M.; Gully, D.; le F
FERS Lett. 317, 139-142, 1993
A;Title: Cloning and expression of a complementary DNA encoding a high affinity human ne
A;Reference number: S29506; MUID:93154505; PMID:8381365
A;Accession: S29506
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-418 <VIT>
A;Cross-references: EMBL:X70070; NID:G35020; PIDN:CAA49675.1; PID:G35021
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.8%; Score 491; DB 2; Length 418;
Best Local Similarity 32.8%; Pred. No. 3.9e-32;
Matches 125; Conservative 62; Mismatches 118; Indels 76; Gaps 13;

QY 39 VPTAVCLCLFVVGSGNVVTVMLIGR---YRDMRTTNLYLGSMVSDLL-ILGLPFD 94
Db 64 VLTVAVTALFVVGTVGNTVTAFTLARKKLSQSLQSTVHYHLSGLSALSDLLTLLAMPVE 123
QY 95 LYR-LWRSRPWFPGPCLCRSLVYGECTATLLHMTALSVERYLALCRPLRARVLVTR 153
Db 124 LYNFIWHPHWFAGDAGCGYFRLDACTATALNVAASLSVERYLALCHPFKATLMRS 183
QY 154 RVRLALIAVLWALLSAGPFLFLVGVQDPGIVSVVPGCLNGTARIASSPLASPLMSRA 213
Db 184 RTKFFISAIWLASALLTVMLFTWG-EQN----- 211
QY 214 PPPSPGPTAPAAALFSRECRPSPAQLGALRVMLWVTT-AYFFLPFLCLSLYGLIGR 272
Db 212 -----RSADGQAGGLVCTPT-IHTATVKVVIQVNTFMSFIFPMVVISVLTIIAN 261
QY 273 ELWSSRPL--RCPAAS-----GREGRHQTKRVLLVVLAFICWLPFHV 316
Db 262 KLTWVRQAEOGVQCTVCGEHSFTSNAIEPGRVQALRHGVRVLRVAVIAFVVCWLPYHV 321
QY 317 GRIIYINTEDSR---MMY-FSQYFNIVALQLFYLASINPILNLYSKKYR-----AA 365
Db 322 RRLMFCYISDEQWTFLEDFYHYFYLMTNALFVSSAINPILNLYSANPRHIFLATLAC 381
QY 366 AFKLLIARKSRPRGFRHSRRT 386
Db 382 LCPVWRRRRKRP-AFSRKADS 401

RESULT 3
JC7913
capa receptor (CG14575) - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 31-Mar-2003 #sequence_revision 31-Mar-2003 #text_change 14-Jul-2003
C;Accession: JC7913
R;Iversen, A.; Cazzamali, G.; Williamson, M.; Hauser, F.; Grimmelikhuijzen, C.J.P.
Biochem. Biophys. Res. Commun. 299, 628-633, 2002
A;Title: Molecular cloning and functional expression of a Drosophila receptor for the ne
A;Reference number: JC7913; MUID:22347021; PMID:12459185
A;Accession: JC7913
A;Molecule type: mRNA
A;Residues: 1-477 <IVE>
A;Cross-references: GB:AF505865
C;Comment: This receptor that is a G-protein-coupled receptor stimulates renal (Malpighi
```

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C;Genetics:
A;Introns: 70/3; 121/2; 126/1; 218/2; 276/2; 301/2; 349/1; 402/3; 436/3
Query Match 20.9%; Score 451; DB 2; Length 477;
Best Local Similarity 29.7%; Pred. No. 7.7e-29;
Matches 117; Conservative 68; Mismatches 135; Indels 74; Gaps 11;

QY 8 SDGPEGAREPPWPAALPPCDERRCSP-----FFLGALVPVTVAVCLCLFVVGVSG 55
Db 30 SDPSHGFGBEDY----ACGTFCNSPKPEFVAVFLGPOTLPYKAVLITIFGGIFITGVWG 85
QY 56 NVVTVMILIGRYDMRTTNLYLGSMVSDLLILL-CLPFDLYLWESRPWVPGPILCRLS 114
Db 86 NLIVCVIIRHSAHMTATNYIFLSAVSOLLVLLFGLTEVELYWHQYFDLFGMPCKR 145
QY 115 LYVGECTYATLLHMTALSVERYLALCRPLRARVLVTRRRVRALIAVLWALLSAGPFL 174
Db 146 AFISEACTYVSFTIVAFSMERFLAICHPLHLVAMVGFKRAIRIITALMIVSFISAFF- 204
QY 175 FLVGVQDPGIVSVVPGCLNGTARIASSPLASPLMSRAPPPSPGPETAEAALFSRE 234
Db 205 -----GLLSDIQYLNLYPLDHS-----RIEESAF----- 227
QY 235 CRPSPAQLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRG--PAASGRERG 292
Db 228 CSMSPKIVNEIPVEVSFCIFVPMILILLYLGRMGAKIRSNRTOKLGVQOQTNNRTR 287
QY 293 HRQTK-----RVLLVVVLAFICWLPFHVGRIIYINTEDSRMVYFSQYFNI-----VAL 341
Db 288 NSQMRKKTIVIRMLAAVITFFVCWFFHLQRLIFLVAKN-----MDNYLDINEALFSIAG 342
QY 342 QLFLYSASINPILNLYSKKYRAAFAFKILLARKS 375
Db 343 FAYVSVCTVNPVIVYSWRRYR-VAFRELLCGKA 375

RESULT 4
A88013
protein K10B4.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: A88013
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biologi
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.eleg
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: A88013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-418 <STO>
A;Cross-references: GR:chr_II; PIDN:AB71009.1; PID:G2429475; GSPDB:GN000020; CESP:K10B4.4
A;Note: similar to family I of G-protein coupled receptors
C;Genetics:
A;Gene: K10B4.4
A;Map position: 2

Query Match 20.1%; Score 434; DB 2; Length 418;
Best Local Similarity 30.1%; Pred. No. 1.6e-27;
Matches 109; Conservative 77; Mismatches 138; Indels 38; Gaps 10;

QY 29 RCSPFPLGALVPVTVAVCLCLFVVGSGNVVTVMLIGRYDMRTTNLYLGSMVSDLL-I 87
Db 24 RCQ--SAGIVPTVIYTGTFILGLDGFNGICTCIVTAANKSMNPTNYILFSLAVSIAL 81
QY 88 LLGLPFDLYR-LWRSRPWFPGPCLCRSLYVGECTATLLHMTALSVERYLALCRPLRA 146
Db 82 ILGLPMEFYQSLDYSYPYRFSGICKARAFLEFTSYASIMILCCSFERLWALCHPLRS 141
QY 147 RVLVTRRRVRALIAVLWALLSAGPFLFLVGVQDP-----GISVVGCLNGTARIASSPJA 203
Db 142 KIPFTLWRANVLIIANTWISTFICALPIAFIVQINKPLPDEKAYQPTNKNVSPFAVGVLN 201
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QY 204 SSPPLWLSRAPPPSPGPTAAALRSREC-----RPSPAQLGALRVMLVWTTTAYFFL 258
Db 202 -----NRIFPV-----TDGIFVLHTEFCAMNQSRPDQOKM-----IIIFAFVTFEVI 244
QY 259 PFLCLISLYGLIGRELWSSRRPLRGP--AASGREGRHRTKRVLLVAVLAFICWLPHVH 316
Db 245 PAIAIVINAHIAVLESEDDKDKVKVKRKNRNLVXKMLSVVITFFICWLPFHI 304
QY 317 GRIIINTEDSRMMYFQYFNIVALQLFYL-----ASINPILYNLISKYRAAFKL 369
Db 305 QRLLSVYTTWSETTITSPVQFLSMIVFISGFCYSNSAANPILYNLISKYSAFCKT 364
QY 370 LL 371
Db 365 IL 366

RESULT 5
S68822
neurotensin receptor 2, leucocastine-sensitive - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 20-Jun-2000
C:Accession: S68822
R:Chalon, P.; Vita, N.; Kaghad, M.; Guillemot, M.; Bonnin, J.; Delpech, B.; le Fur, G.;
FEBS Lett. 386, 91-94, 1996
A:Title: Molecular cloning of a leucocastine-sensitive neurotensin binding site.
A:Reference number: S68822; MUID:96228041; PMID:8647296
A:Accession: S68822
A:Molecule type: mRNA
A:Residues: 1-416 <CHA>
A:Cross-references: GB:X97121; NID:g1483579; PIDN:CAA65787.1; PID:g1483580
A:Experimental source: hypothalamus
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:33-58/Domain: transmembrane #status predicted <TM1>
F:70-91/Domain: transmembrane #status predicted <TM2>
F:110-131/Domain: transmembrane #status predicted <TM3>
F:154-175/Domain: transmembrane #status predicted <TM4>
F:204-230/Domain: transmembrane #status predicted <TM5>
F:296-315/Domain: transmembrane #status predicted <TM6>
F:335-361/Domain: transmembrane #status predicted <TM7>

Query Match 18.6%; Score 401; DB 2; Length 416;
Best Local Similarity 29.4%; Pred. No. 7, 3e-25;
Matches 122; Conservative 68; Mismatches 145; Indels 80; Gaps 13;

QY 18 PWPALP-----PDERCSPPLGALVPVTVAVCLCLFVWVGSGNVVTVMLIGRYDMRT 71
Db 6 PWPFRPSPSAGLSLEARLGVDTLWAKVLTALYSLIFAFAGTAGNALSVHVVVKARAGRP 65
QY 72 -TTNLYLGSMVSDLLIL-GLPELDLR-LWRSRPWFVGPFLCLRLSLVVGEGCTVATLH 128
Db 66 GLRLYHVLALSAALLLVLVSMPELMYFNVSHYVWFGDLGCRGYFVRELCAVATVLS 125
QY 129 MTALSVERYLALCPRLARVLVTRRRVALLAVLWALLSAGPFLFVLGV-----179
Db 126 VASLSAERCLAVCQPLRARRLLTPRTRLLSLVWVSLGLALPMVIMGQKHEVESADG 185
QY 180 EQDPCISVVPGLNGTARIA-----SSPLASSPFLMSRAPPPSPGPTAA 228
Db 186 EPEPASRVCTVLVSRATLQVFTQVNLVSVFALPLALTAF-----NGITVNLH 234
QY 229 ALFSRECRPSPAQLGALRVMLVWTTTAYFFLPLCLISLYGLIGRELWSSRRPLRGPASG 288
Db 235 ALYS-QVFSAGAQSISPSRELGE-----EGLLGFTWRTKTLUSLGVSQASLV 281
QY 289 PERGHRQTK-----RVLLVVVLAFLICWLPHVGRITVINTED-----SRMMYFQYFNI 338
Db 282 RHKDAQSLRSLQHSQAQLRAIVAVVVCWLPVHARLMYCIYIPDDGTWNLVDFHYFYM 341
QY 339 VALQFLYLSASINPILYNLISKYRAAFKLARKSRPRGFRHSRDTAGEVAGD 393
Db 339 VALQFLYLSASINPILYNLISKYRAAFKLARKSRPRGFRHSRDTAGEVAGD 393

Db 342 VNTLFFYVSSAVTPILYNAVSSFR-----KULFL-----ESLGLSCGE 379

RESULT 6
T15816
hypothetical protein C48C5.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C:Accession: T15816
R:Favell, A.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C48C5.
A:Reference number: Z18410
A:Accession: T15816
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-378 <FAV>
A:Cross-references: EMBL:U39994; NID:g1055102; PID:g1055105; PIDN:AAB37017.1; GSPDB:GNO(C
A:Experimental source: strain Bristol N2; clone C48C5
C:Genetics:
A:Gene: CESP:C48C5.1
A:Map position: X
A:Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1; 327/1
C:Superfamily: adenosine receptor A1

Query Match 17.5%; Score 378; DB 2; Length 378;
Best Local Similarity 28.7%; Pred. No. 4, 8e-23;
Matches 97; Conservative 70; Mismatches 135; Indels 36; Gaps 9;

QY 38 LVPVTAVCLCFVVGSGNVVTVMLIGRYDMRTTNLYLGSMVSDLLIL-LGPELDLY 96
Db 51 LYKVTALYIFFLVGVIGVNTTCLVMKHPMKTHASMLWNLAVSDLVTLVCGLPFVW 110
QY 97 RLWRSRPWFVGPFLCLRLSLVVGEGCTVATLHMTALSVERYLALCPRL-RARVLVTRRV 155
Db 111 MNWQYPPWFPDYICNLKALIAETTSVSILTILFALERYVAVVCHPLFLMKVQPFKNI 170
QY 156 RALTAVLWAVALLSAGPFLFVLGVGEQDGISSVPLNGTARIASSPLASSPFLMSRAP 215
Db 171 GTIIGFTWIFSLCAMP--FAIHRADYIMKSWPQDNRIPVSKSKCM-----217
QY 216 PSPSPGPETAABAAALFSRECRPSPAQLGALRVML-VWTTAYFFLPLCLISLYGLIGREL 274
Db 218 -----IAYNF-----EPKLASTFKILPHFSAIFALPLFTIVILYARIACKV 260
QY 275 WSSRRPLRGPASGRGRHRTKRVLLVWVLAFLICWLPHVGRITVINTEDSRMM-YFS 333
Db 261 -SSNRTIQPGELDITEELQMRINAILCAIVSAFFICVLPQLRLFFVFDNEVILTVN 319
QY 334 QYFNIVALQLFYLGSINPILYNLISKYRAAFKL 371
Db 320 QYMFISGLFYLATIIINPIAYNLASSRFR-RAFKDIL 356

RESULT 7
157940
somatostatin receptor 5 - rat
N:Alternate names: somatostatin release-inhibiting factor subtype 28 receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999
C:Accession: 157940; 157949; S39244
R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 42, 939-946, 1992
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A:Reference number: 157940; MUID:93125499; PMID:1362243
A:Accession: 157940
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-363 <OCAL>
A:Cross-references: GB:I04535; NID:g409238; PIDN:AAA17029.1; PID:g409239
R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
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A;Reference number: I57949; MUID:94088493; PMID:8264565
A;Accession: I57949
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 341-363 <OCA2>
A;Cross-references: GB:S67370; NID:g455947; PIDN:AAB29371.1; PID:g455948
A;Experimental source: pituitary
R;Panetta, R.; Greenwood, M.; Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A;Description: Correction of the nucleotide and amino acid sequence of the rat somatostatin
A;Reference number: S39244
A;Accession: S39244
A;Molecule type: mRNA
A;Residues: 309-363 <PEN>
A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
C;Genetics:
A;Gene: SSTR5
C;Superfamily: vertebrate rhodopsin

Query Match          16.6%; Score 358; DB 2; Length 363;
Best Local Similarity 27.3%; Pred. No. 1.9e-21;
Matches 110; Conservative 60; Mismatches 149; Indels 84; Gaps 12;

QY 5 WNGSDGPEGAREPPWALPPCDERRCSPFPLGA---LVPVTAVCLCLFVVGSGNVVTVM 61
DB 12 WNASAASGNHN--WSLVG-----SASPMGARAVLPVLYLLVC--TVGLSGNTLVIY 60

QY 62 LIGYRDMRTTNLYLGSMAVSDLLIILGLPFDLYRLWRSPWVFGPLCLRLSLYVGECC 121
DB 61 VULRHAKMKTVTNYIILNLAADVLFMLGLPFLATONAVSVYFPGSLCRLVMTLDGIN 120

QY 122 TYATLLHMTALSYERYLAI CRPLRARVLVTRRRVRALIAVLMAVALLSAGFFLVGVEQ 181
DB 121 QFTSIFCLMWSDVRYLAVVHPFLBSARWRPRVAKASAAVWFSLSMLPLLVADVQEE 180

QY 182 DPGISVVGGLNGTARIASSPLASSPPLWLSRAPPSPPGPETAEEAALFSRECRPSAQ 241
DB 181 G-----WGTCNLS-----W-----PEPVG 194

QY 242 LGLARVLMWTTAYFFLPFLCLSLYGLI-----GRELWSSRRPLRGPAASGRGRCHR 294
DB 195 LWGAFTYTSVGLGFFGLPLVICLYLLIVVKKAAGRVGSSR-----RRRSEP 244

QY 295 QTKRVLIVVLAFTICMLPFHVGRRIIYIN-TEDSRMMYFQYENIVALQLFYLSSINPI 353
DB 245 KVTSMVVVVVLFVFGWLPFFIVNVLAFTLPDEPTSAGLYFVVVLS--YANSCANPL 302

QY 354 LYNLISKYRAAFAFKLLARKSRPRGHRSDRTAGEVAGDTGG 396
DB 303 LYGLSDNFRQSRFKVLCRLR---RGYGMEDADAIEPRPKSG 341

RESULT 8
A46226
somatostatin receptor 3 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
R;Accession: A46226; S32501
R;Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Seino, M.; Endocrinol. 6, 2136-2142, 1992
A;Title: Somatostatin receptors, an expanding gene family: cloning and functional charac
A;Reference number: A46226; MUID:93149123; PMID:1337145
A;Accession: A46226
A;Molecule type: DNA
A;Residues: 1-418 <MAN>
A;Cross-references: GB:M96738; NID:g338498; PIDN:AAA60592.1; PID:g338499
A;Note: sequence extracted from NCBI backbone (NCBIN:1233685, NCBI:P123690)
R;Corness, J.D.; Demchishyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent, G.; FEBS Lett. 321, 279-284, 1993
A;Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays preferential binding to [D-Trp6]somatostatin
A;Reference number: S32501; MUID:93238970; PMID:8097479
A;Accession: S32501
A;Status: preliminary
A;Gene: GDB:SST

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A;Molecule type: DNA
A;Residues: 1-418 <COR>
C;Genetics:
A;Gene: GDB:SSTR3
A;Cross-references: GDB:134187; OMIM:182453
A;Map position: 22q13.1-22q13.1
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;44-70/Domain: transmembrane #status predicted <TM1>
F;81-106/Domain: transmembrane #status predicted <TM2>
F;118-139/Domain: transmembrane #status predicted <TM3>
F;159-181/Domain: transmembrane #status predicted <TM4>
F;203-233/Domain: transmembrane #status predicted <TM5>
F;255-282/Domain: transmembrane #status predicted <TM6>
F;289-316/Domain: transmembrane #status predicted <TM7>
F;17,30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;116-191/Disulfide bonds: #status predicted
F;151,251,317,332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;251/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted
F;256/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predicted
F;412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match          16.5%; Score 356.5; DB 2; Length 418;
Best Local Similarity 26.3%; Pred. No. 2.9e-21;
Matches 101; Conservative 63; Mismatches 146; Indels 65; Gaps 10;

QY 11 PEGAREPPWALPPCDERRCSPFPL-----GALVPVTAVCLCLFVVGSGNVVTVM LIGR 65
DB 15 PENA-SSAMPDPATLGNVSAGSPAGLAVSGVLPLVYLVC--VVGLLGNLSLVIYVLR 71

QY 66 YRDMRTTNLYLGSMAVSDLLIILGLPFDLYRLWRSPWVFGPLCLRLSLYVGECCYAT 125
DB 72 HTASPSVTNYIILNLADELFLMLGLPF-LAAQNALSYNPFGLSLMCLVMAVDGINQFTS 130

QY 126 LLHMTALSYERYLAI CRPLRARVLVTRRRVRALIAVLMAVALLSAGFFLVGVEQDQGI 195
DB 131 IFCLTWSVDVRYLAVVHPFTRSAWRTPAVRTVSAVAVVAVVLFVVVFSVGV----- 184

QY 186 SVVPGGLNGTARIASSPLASSPPLWLSRAPPSPPGPETAEEAALFSRECR---PSPAQL 242
DB 185 -----PRGMST-----CHMQWPEPAAA 201

QY 243 GALTVMWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTKRVLLV 302
DB 202 WRAGFIITYTAALGFFGFLPLVICLYLLIVVKSAGRYVWAPSQQRRRSRRVTRMVVA 261

QY 303 VLAFTICMLPFHVGRRIIYINTE-DSRMMYFQYENIVALQLFYLSSINPIYNLISKX 361
DB 262 VVALFVLCWMPFYVLNVNVVCPLEPPEAFGLYFLVVALP--YANSCANPILYGLFSYR 319

QY 362 YRAAFAFKLLARKSR 376
DB 320 FK-QGFRVLLRPSR 333

RESULT 9
I57955
somatostatin receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
R;Panetta, R.; Greenwood, M.T.; Warszynska, A.; Demchishyn, L.L.; Day, R.; Niznik, H.B.; Mol. Pharmacol. 45, 417-427, 1994
A;Title: Molecular cloning, functional characterization, and chromosomal localization of
A;Reference number: I57955; MUID:94195267; PMID:7908405
A;Accession: I57955
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-363 <RES>
A;Cross-references: GB:L14865; NID:g431094; PIDN:AAA20828.1; PID:g431095
C;Genetics:
A;Gene: GDB:SST

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A;Cross-references: GDB:119604; OMIM:182450
 A;Map position: 3q28-3q28
 C;Superfamily: vertebrate rhodopsin

Query Match 15.9%; Score 343; DB 2; Length 363;
 Best Local Similarity 27.7%; Pred. No. 3.1e-20;
 Matches 106; Conservative 58; Mismatches 131; Indels 88; Gaps 14;
 QY 14 AREPPNPALPP-----CDERR-CSPEP-LGA-----LVPVTAVCLCLFVVGSGNVTVM 62
 Db 7 ASTPSWNASPGGAASGGDNRTLVPAPSAGARAVLPVLLVC--AAGLGGNTLVIYV 64
 QY 63 IGRYDRMTTNYLYGSMVSDLLILGLPDLRLWRSRPFVGLLCLRLSLYVGGCT 122
 Db 65 VLRFKMTVTNYILNLAVADVLYMLGLPP-LATQNAASFMPFPGVLCRLVMTLDGVNQ 123
 QY 123 YATLLHMTALSVRYLAICRPLARVLTTRRRVALLAVLMAVALLSAGPFLFVGVQED 182
 Db 124 FTSVFCITVMSVDRLAVVHPLSARWRPRVAKLAGAAVLSCLMSLPFLVADVQE- 182
 QY 183 PGISVWPLNGTARIASSPLASPPMLSRAPPPSPGPETAFAALFSRECRPSAQL 242
 Db 183 -----GTCNAS-----W-----PEPVG 196
 QY 243 GALTVMVLTATYFFLPFLCLSLIYGLIGRELSSRRPLRGPASG-----RRGHQT 296
 Db 197 WGAVFIIYTVLGFAPLLVICLCYLLIVKV-----RAAGVRVGCVRRSERKV 246
 QY 297 KRVLVVVLAFLICWLPFHVGRIYI-----NTEDSRMYFSQVFNIVALQFLYLSASIN 351
 Db 247 TRVLVVVLVFGCWLFPFTVINVLAVLPQEPASAGLYF---FVVI---LSYANSCAN 300
 QY 352 PILYNLISKYRAAFAKLLARK 374
 Db 301 PVLYGFLSDNFRSQFQVLCIRK 323

RESULT 10

JN0763
 somatostatin receptor 5 - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
 C;Accession: JN0763
 R;Yanada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
 Biochem. Biophys. Res. Commun. 195, 844-852, 1993
 A;Title: Cloning, functional expression and pharmacological characterization of a fourth
 A;Reference number: JN0762; MUID:93384611; PMID:8373420
 A;Accession: JN0763
 A;Molecule type: DNA
 A;Residues: 1-364 <YAM>
 A;Cross-references: DDBJ:D16827; NID:g487683; PIDN:BA04107.1; PID:g487684
 C;Comment: This protein is a member of somatostatin receptor family.
 C;Genetics:
 A;Gene: GDB:SSTR5
 A;Cross-references: GDB:138452; OMIM:182455
 A;Map position: 16p13.3-16p13.3
 A;Introns: #status absent
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; thiol
 F;40-66/Domain: transmembrane #status predicted <TM1>
 F;77-102/Domain: transmembrane #status predicted <TM2>
 F;114-135/Domain: transmembrane #status predicted <TM3>
 F;155-177/Domain: transmembrane #status predicted <TM4>
 F;196-228/Domain: transmembrane #status predicted <TM5>
 F;246-273/Domain: transmembrane #status predicted <TM6>
 F;280-307/Domain: transmembrane #status predicted <TM7>
 F;13,26,187/Binding site: carbohydrate (Aen) (covalent) #status predicted
 F;112-186/Disulfide bonds: #status predicted
 F;242,325/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pred
 F;247/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic
 F;320/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 15.9%; Score 343; DB 2; Length 364;

Best Local Similarity 27.7%; Pred. No. 3.1e-20;
 Matches 106; Conservative 58; Mismatches 131; Indels 88; Gaps 14;
 QY 14 AREPPNPALPP-----CDERR-CSPEP-LGA-----LVPVTAVCLCLFVVGSGNVTVM 62
 Db 7 ASTPSWNASPGGAASGGDNRTLVPAPSAGARAVLPVLLVC--AAGLGGNTLVIYV 64
 QY 63 IGRYDRMTTNYLYGSMVSDLLILGLPDLRLWRSRPFVGLLCLRLSLYVGGCT 122
 Db 65 VLRFKMTVTNYILNLAVADVLYMLGLPP-LATQNAASFMPFPGVLCRLVMTLDGVNQ 123
 QY 123 YATLLHMTALSVRYLAICRPLARVLTTRRRVALLAVLMAVALLSAGPFLFVGVQED 182
 Db 124 FTSVFCITVMSVDRLAVVHPLSARWRPRVAKLAGAAVLSCLMSLPFLVADVQE- 182
 QY 183 PGISVWPLNGTARIASSPLASPPMLSRAPPPSPGPETAFAALFSRECRPSAQL 242
 Db 183 -----GTCNAS-----W-----PEPVG 196
 QY 243 GALTVMVLTATYFFLPFLCLSLIYGLIGRELSSRRPLRGPASG-----RRGHQT 296
 Db 197 WGAVFIIYTVLGFAPLLVICLCYLLIVKV-----RAAGVRVGCVRRSERKV 246
 QY 297 KRVLVVVLAFLICWLPFHVGRIYI-----NTEDSRMYFSQVFNIVALQFLYLSASIN 351
 Db 247 TRVLVVVLVFGCWLFPFTVINVLAVLPQEPASAGLYF---FVVI---LSYANSCAN 300
 QY 352 PILYNLISKYRAAFAKLLARK 374
 Db 301 PVLYGFLSDNFRSQFQVLCIRK 323

RESULT 11

A55259
 kappa opioid receptor - guinea pig
 N;Alternate names: dynorphin receptor
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-Nov-1999
 C;Accession: A55259
 R;Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A.; Watson
 Proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994
 A;Title: Primary structure and functional expression of a guinea pig kappa opioid (dynor
 A;Reference number: A55259; MUID:9424825; PMID:8170987
 A;Accession: A55259
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-380 <XTE>
 A;Cross-references: GB:U04092; NID:g476106; PIDN:AAA67171.1; PID:g476107
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: transmembrane protein

Query Match 15.9%; Score 342.5; DB 2; Length 380;
 Best Local Similarity 25.1%; Pred. No. 3.6e-20;
 Matches 102; Conservative 74; Mismatches 147; Indels 83; Gaps 12;
 QY 2 GSPW-----NGSDGPEGAREPP---WPAIPCCDERRCSPFPLGALVPVTAVCLCLF 49
 Db 26 GSAWLPQWAPDNGSAGPQDEQLEPAHISPAIP-----VIITAVYSVVF 70
 QY 50 VVGSGNVVTVMILIGRYDRMTTNYLYGSMVSDLLILGLPDLRLWRSRPFVGL 109
 Db 71 VVGLVGSNVFVIIRTKMTATNYIIFNLADALVTTMTMPFQ-STVIMNSWPGDV 129
 QY 110 LCRSLYVGGGCTYATLLHMTALSVRYLAICRPLARVLTTRRRVALLAVLMAVALLS 169
 Db 130 LCKIVISIDYNNFTSIFTLTMSVDRIYAVCHPVKALDFRPLKAKIINICIWLLSSSV 189
 QY 170 AGFPLFVGVQDPGIVSVPLNGTARIASSPLASPPMLSRAPPPSPGPETAFAA 229
 Db 190 GISAILLGGTKVRDVEDIIE-----CSLQFPDDDDYSWD----- 223
 QY 230 LFSRECRPSAQLGALRVMLVVTATYFFLPFLCLSLIYGLIGRELSSRRPLRGPASGR 289


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Db      224 LFMKIC-----VFVEAFVIVPVLIIIVCYTLMILRL-KSVRLLSG--SREK 265
QY      290 ERGRQTKRVLLVVLVLAFLICWIPFHVGRILYI--NTEDSRMMYFQYQFNIVALQFLYLS 347
Db      266 DRNLRLTRVLVVVAVFIICWIPFHIFILVEALGSTSHSTAALSSVYF---CIALGYTN 322
QY      348 ASINPILYNLISKYRAA-----AFKLLARKSRPRGFRHSRDTA 387
Db      323 SSLNPILYAFLDENFRCRFDRCFFPKRMERGSTSRVRNTVQDPA 369

RESULT 12
JE0296
thyrotropin releasing hormone receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C:Accession: JE0296
R;Itadani, H.; Nakamura, T.; Itoh, J.; Iwaasa, H.; Kanatani, A.; Borkowski, J.; Ihara, M
Biochem. Biophys. Res. Commun. 250, 68-71, 1998
A;Title: Cloning and characterization of a new subtype of thyrotropin-releasing hormone
A;Reference number: JE0296; MUID:98407892; PMID:9735333
A;Accession: JE0296
A;Molecule type: mRNA
A;Residues: 1-352 <ITA>
A;Cross-references: DDBJ:AB015645; NID:G3660553; PIDN:BAA33437.1; PID:G3660554
C;Superfamily: adenosine receptor A1
F;26-48/Domain: transmembrane #status predicted <TM1>
F;58-80/Domain: transmembrane #status predicted <TM2>
F;97-118/Domain: transmembrane #status predicted <TM3>
F;142-165/Domain: transmembrane #status predicted <TM4>
F;188-209/Domain: transmembrane #status predicted <TM5>
F;252-273/Domain: transmembrane #status predicted <TM6>
F;282-304/Domain: transmembrane #status predicted <TM7>

Query Match      15.7%; Score 338; DB 2; Length 352;
Best Local Similarity 28.8%; Pred. No. 7.6e-20;
Matches 108; Conservative 52; Mismatches 109; Indels 106; Gaps 13;

QY      41 VTAVCLCLFV--VGSGNVVTVMLIGRYDRMTTTLNLYGSMVAVSLLILL--GLPFDLY 96
Db      23 VVSFVLVLVCTLGIIGNAMVILVITSRDMHTPTNCYLVSALADLLVLAAGLNVSD 82
QY      97 RLWRSPVFGPLLCRLSLVYVGCGTYATLL-----HMTLSVERYLAICRPLRARVL 149
Db      83 SL--VGHWIYGRAGL-----GITYFQYLGINVSFSILFTVERYIAICHPLAQTV 133
QY      150 VTRRRVRLAIVLAWALLSAGFLFLVGV-----EQDPSIVVPLGNTARIASPLA 203
Db      134 CTVARAKRIAGIWGVTSLYCLLWFLVDLNVDRNORLECGYKVPRL-----181
QY      204 SSPPLWLSRAPPPSPGPTAEAAALFSRECRPSAQLGALRVLWVTTAYFFLPFLCL 263
Db      182 -----YLPYLLDFAVFPIGLVLT 201
QY      264 SILYGLIGR-----ELWSSRRPLRG--PAASGR-----ERGHQTKRVLLVVLVLAFL 308
Db      202 LVLYGHIGRILFQSPLSQEAQKQERPHGQSEAPGNCRAKSRKQATRLAVVVLLEA 261
QY      309 ICWLPFHVGRILYIINTEDSRMMYFQYQFNIVALQLF-----YLSASINPLYNLISKYR 363
Db      262 VLTPTPT--LVLLNS-----FVAQFLDPWLLFCRTCVTNSAVNPVYVSLMSQKR 313
QY      364 AAAPKLLARKSRPR 378
Db      314 AAFKLKCWCAAGPQ 328

RESULT 13
S36143
kappa opioid receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Dec-1993 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000
C:Accession: S36143; S38825; S36102; S39015; A48789

```

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R;Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K.
FEBS Lett. 330, 77-80, 1993
A;Title: cDNA cloning and pharmacological characterization of an opioid receptor with hig
A;Reference number: S36143; MUID:93380575; PMID:8396539
A;Accession: S36143
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-380 <NIS>
A;Cross-references: GB:D16534; NID:G409390; PIDN:BAA03971.1; PID:G415310
R;Chen, Y.; Mestek, A.; Liu, J.; Yu, L.
Biochem. J. 295, 625-628, 1993
A;Title: Molecular cloning of a rat kappa opioid receptor reveals sequence similarities t
A;Reference number: S38825; MUID:94059008; PMID:8240267
A;Accession: S38825
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-380 <CHE>
A;Cross-references: GB:L22001; NID:G409236; PIDN:AAA41495.1; PID:G409237
R;Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.; Onogi, T.; Kaneko, S.; Satc
FEBS Lett. 329, 291-295, 1993
A;Title: Cloning and expression of a cDNA for the rat kappa-opioid receptor.
A;Reference number: S39015; MUID:94059009; PMID:8240268
A;Accession: S39015
A;Molecule type: mRNA
A;Residues: 1-344, 'Y', 346-380 <LIS>
A;Cross-references: GB:L22536; NID:G425188; PIDN:AAA41496.1; PID:G425189
R;Meng, F.; Xie, G.
Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958, 1993
A;Title: Cloning and pharmacological characterization of a rat kappa opioid receptor.
A;Reference number: A48789; MUID:94052210; PMID:8234341
A;Accession: A48789
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-380 <RES>
A;Cross-references: EMBL:U00442; NID:G403486; PIDN:AAA18261.1; PID:G403487
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

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Query Match      15.7%; Score 338; DB 2; Length 380;
Best Local Similarity 25.5%; Pred. No. 8.2e-20;
Matches 103; Conservative 75; Mismatches 146; Indels 80; Gaps 13;

QY      6 NGSQDGPGEAREPP---WPALPPCDERRCSFFPLGALVPVTVAVCLCLFYVYVSGNVVTVML 62
Db      39 NGSVSGEDQQLPEAHISPAIP-----VIITAVSVVVFVGLVGNLSWVF 83
QY      63 IGRYDRMTTTLNLYGSMVAVSLLILLGLPFLRLWRSPVWFGPLLCRLSLYVGEGET 122
Db      84 IIRYTKMKATNIYIFNLALADALVTTMFFQ--SAVYLMNSWPFQGVLCXIVISIDYNN 142
QY      123 YATLHMTALSVERYLAICRPLRARVLVTRRRVRLAIVLWAVALLSAGFLFLVGVQED 182
Db      143 FTSIFTLTMSVDRYIAVCHPVKALDFRPLKAKTINICIMLLASSVGSIAIVLGGTKVR 202
QY      183 PGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRSPALQ 242
Db      203 EDVDVIE-----CSIQFPDDDEYSWMD-----LFMKIC-----229
QY      243 GAIKRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHQTKRVLLV 302
Db      230 -----VFVFAFVIVPVLIIIVCYTLMILRL-KSVRLLSG--SREKQNLRIITKVLV 278
QY      303 VVLAFLICWLPFHVGRILYI--NTEDSRMMYFQYQFNIVALQFLYLSASINPLYNLISK 360
Db      279 VVAVFICTWPTPIHIFLVEALGSTSHSTAALSSVYF---CIALGYTNLSNLPVLAFLDE 335

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```
QY      361 KYRAA-----AFKLLARKSRGPHRSRDTAGEVAG--DTGG 396
      : : : : : : : : : : : : : : : : : : : : : :
Db      336 NFKRCFRDFCFPIKRMEROST-----NRVNTVQDPASMRDVG 375
      : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
JC2338
kappa opioid receptor 1 - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 19-May-2000
C;Accession: JC2338; A55354; I57005; G01546
R;Mansson, E.; Bare, L.; Yang, D.
Biochem. Biophys. Res. Commun. 202, 1431-1437, 1994
A;Title: Isolation of a human kappa opioid receptor cDNA from placenta.
A;Reference number: JC2338; MUID:94338360; PMID:8060324
A;Accession: JC2338
A;Molecule type: mRNA
A;Residues: 1-380 <MAN>
A;Cross-references: GB:U11053; NID:G532059; PIDN:AAA20985.1; PID:G532060
A;Experimental source: Placenta
R;Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.
J. Biol. Chem. 269, 25966-25969, 1994
A;Title: Human kappa opiate receptor second extracellular loop elevates dynorphin's affinity
A;Reference number: A55354; MUID:95014415; PMID:7929306
A;Accession: A55354
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 136-279 <MAN>
A;Cross-references: GB:I36130; NID:G598184; PIDN:AAA63646.1; PID:G598185
R;Zhu, J.; Chen, C.; Xue, J.
Life Sci. 56, 201-207, 1995
A;Title: Cloning of a human .kappa. opioid receptor from the brain.
A;Reference number: I57005
A;Accession: I57005
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1, 'D', 3-380 <ZHU>
A;Cross-references: GB:I37362; NID:G722617; PIDN:AAA63906.1; PID:G722618
R;Grandy, D.K.
submitted to the EMBL Data Library, November 1994
A;Reference number: G07718
A;Accession: G01546
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 132-203 <GRA>
A;Cross-references: EMBL:U16860; NID:G595932; PIDN:AAA56758.1; PID:G595933
C;Comment: This receptor preferentially binds dynorphins.
C;Genetics:
A;Gene: GDB:OPRK1; KOR
A;Cross-references: GDB:132651; OMIM:165196
A;Map position: 8q11.2-8q11.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; receptor; transmembrane protein
F;60-85/Domain: transmembrane #status predicted <TM1>
F;95-114/Domain: transmembrane #status predicted <TM2>
F;133-154/Domain: transmembrane #status predicted <TM3>
F;177-199/Domain: transmembrane #status predicted <TM4>
F;228-251/Domain: transmembrane #status predicted <TM5>
F;275-296/Domain: transmembrane #status predicted <TM6>
F;311-333/Domain: transmembrane #status predicted <TM7>

Query Match      15.5%; Score 334; DB 2; Length 380;
Best Local Similarity 25.2%; Pred. No. 1.7e-19;
Matches 99; Conservative 74; Mismatches 146; Indels 74; Gaps 11;

QY      6 NGSQDGEAREPP---WPALPPCDERRCSFFPLGALVPVTAVCLCFVVGSGNVVWML 62
      : : : : : : : : : : : : : : : : : : : : : :
Db      39 NGSAGSDAQLEPAHISPAIP-----VIITAYSVFVVGILGNSLIVFV 83
      : : : : : : : : : : : : : : : : : : : : : :

QY      63 IGRYDMRTTNLYLGSMAVSDLLILLGLPDLRLWRSPVWFGLLICRLSLYVGEGCT 122
      : : : : : : : : : : : : : : : : : : : : : :
Db      84 IIRYTKMTATNIYIFNLADALVTTTPFQ-STVYLMNSWPFPGDLCKIVISIDYNNM 142
      : : : : : : : : : : : : : : : : : : : : : :
```

```
QY      123 YATLLHMTALSVRYLAICRPLRVLVTRRRRVRLIAVLWAVALLSAGPFLFLVGVQD 182
      : : : : : : : : : : : : : : : : : : : : : :
Db      143 FTSIFTLTMMSDRYIAVCHPVKALDFRPLKAKIINICIMLSSSVGISAIVLGGTKVR 202
      : : : : : : : : : : : : : : : : : : : : : :

QY      183 PGISVVPGLNGTARIASSPLASSPFWLSRAPPPSPSGPETAAALFRRRCRPSAQL 242
      : : : : : : : : : : : : : : : : : : : : : :
Db      203 EDVDVIE-----CSLQFFDDDDYSWMD-----LFMKIC----- 229
      : : : : : : : : : : : : : : : : : : : : : :

QY      243 GALLRVLMTVTTAFYFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRQTKRVLY 302
      : : : : : : : : : : : : : : : : : : : : : :
Db      230 -----VFIFAFVLPVLIIVCYITMLRL-KSVLLSG--SRKDRMLRITRLVIV 278
      : : : : : : : : : : : : : : : : : : : : : :

QY      303 VLAFTICWLPHVGRRIYI--NTDSRMVYFQYFNIVALQLFYLSASINPILYNLISK 360
      : : : : : : : : : : : : : : : : : : : : : :
Db      279 VVAVFVVCWTFIHIFILVEALGSTSHSTAALSSYF--CIALGYTNSSLNPLIYAFLE 335
      : : : : : : : : : : : : : : : : : : : : : :

QY      361 KYRAA-----AFKLLARKSRGPHRSRDTA 387
      : : : : : : : : : : : : : : : : : : : : : :
Db      336 NFKRCFRDFCFPLKRMERQSTSRVENTVQDPA 368
      : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
JN0605
somatostatin receptor 4 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: JN0605; A47457
R;Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A;Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A;Reference number: JN0605; MUID:93290656; PMID:8512564
A;Accession: JN0605
A;Molecule type: DNA
A;Residues: 1-388 <XUY>
A;Cross-references: GB:I14856; NID:G292499; PIDN:AAA36623.1; PID:G292500
R;Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A;Title: Cloning, functional expression and pharmacological characterization of a fourth
A;Reference number: JN0762; MUID:93384611; PMID:8373420
A;Accession: JN0762
A;Molecule type: DNA
A;Residues: 1-388 <YAM>
A;Cross-references: GB:D16826; NID:G693907; PIDN:BAA04106.1; PID:G693908
R;Kohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schule, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A;Title: Cloning and characterization of a fourth human somatostatin receptor.
A;Reference number: A47457; MUID:93248256; PMID:8483934
A;Accession: A47457
A;Molecule type: DNA
A;Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROH>
A;Cross-references: GB:L07833; NID:G307429; PIDN:AAA60565.1; PID:G307430
A;Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBI:P:130856)
C;Comment: This protein mediates the diverse actions of the tetradecapeptide somatostatin.
C;Genetics:
A;Gene: GDB:SSR4
A;Cross-references: GDB:202662; OMIM:182454
A;Map position: 20p11.2-20p11.2
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; ph
F;47-73/Domain: transmembrane #status predicted <TM1>
F;84-109/Domain: transmembrane #status predicted <TM2>
F;121-142/Domain: transmembrane #status predicted <TM3>
F;162-184/Domain: transmembrane #status predicted <TM4>
F;208-238/Domain: transmembrane #status predicted <TM5>
F;257-284/Domain: transmembrane #status predicted <TM6>
F;291-314/Domain: transmembrane #status predicted <TM7>
F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-199/Disulfide bonds: #status predicted
F;161,253/Binding site: phosphate (Ser) (covalent) #status predicted
F;327/Binding site: palmitate (Cys) (covalent) #status predicted
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Query Match      15.5%; Score 334; DB 2; Length 388;
Best Local Similarity 26.9%; Pred.No.1.8e-19;
Matches 105; Conservative 65; Mismatches 128; Indels 92; Gaps 15;

Qy      1 MGSPW---NGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCLCLFVVGVSGN 56
Db      15 LGTAWPSAANASSAPAEAE---AVAGFGDAR-----AAGWVAIQCIYALVCLVGLVGN 65

Qy      57 VVTVMILGRYRDMKTTNNLYIGSMVSDLLILLGLPFDLYRLMRSRPWFPGPLLCRLSLY 116
Db      66 ALVIFVILRYAKMKTATNIYLLNLAVALDELFMLSVPF-VASSAALRHWPFGSVLCRAVLS 124

Qy      117 VGEGETATLLHMTALSVERYLAICRPLRARVLYTRRR--VRALIIV-LWAVALLSAGPF 173
Db      125 VDGLNMFISVFCCLTVLSVDRIYVAVVHPLRA---ATYRRPSVAKLINLGWMLASLLVTLPI 181

Qy      174 LFLVGVBDPFGISVYVPGINGTARIASSPLASSPPLMLSRAPPPSPSGPETAEAAALFSR 233
Db      182 AIFADTR-----PARGGQA--VACNLQWHPFAM-----SAVF-- 211

Qy      234 ECRPSAQLGALRVMLVMTTAYFPLPFLCLSLYGLIGREL-----WSSRRPLRGPA 285
Db      212 -----VVYTFLLGFLPVLATGLCYLLIVGKRAVALRAGWQQR----- 251

Qy      286 ASGRERGHROTQRVLLVVLAFIICWLPFHVGRV--IVINTEDSRMMYFSQYENIVALQL 343
Db      252 -----RSEKKITRLVLMVVVVVFLCWMPFFYVQVLLNLVVISLDATV-----NHVSLIL 299

Qy      344 FYLSASINPILYNLIISKYRAAFKLLAR 373
Db      300 SYANSCANPILYGFSLDNFRRSFORVLCRLR 329
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Search completed: July 4, 2004, 03:10:54
Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2004, 21:29:27 ; Search time 18 Seconds

(without alignments)
1191.828 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPWNGSDGEGAREPPWP.....DTGGDTVGYTETSANVKTMG 412

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2149	99.7	412	1	MTLR_HUMAN
2	858.5	39.8	366	1	GHSR_PIG
3	857.5	39.8	366	1	GHSR_HUMAN
4	855.5	39.7	364	1	GHSR_RAT
5	614	28.5	257	1	GHSR_MOUSE
6	498	23.1	424	1	NTR1_RAT
7	495.5	23.0	424	1	NTR1_MOUSE
8	491	22.8	418	1	NTR1_HUMAN
9	451	20.9	477	1	CAPR_DROME
10	407	18.9	410	1	NTR2_HUMAN
11	404	18.7	417	1	NTR2_MOUSE
12	401	18.6	416	1	NTR2_RAT
13	369.5	17.1	362	1	SSR5_MOUSE
14	358	16.6	363	1	SSR5_RAT
15	355.5	16.5	418	1	SSR3_HUMAN
16	349.5	16.2	453	1	GP39_HUMAN
17	343	15.9	364	1	SSR5_HUMAN
18	342.5	15.9	380	1	OPRK_CAVPO
19	341.5	15.8	370	1	OPRK_CAVPO
20	338	15.7	380	1	OPRK_RAT
21	334	15.5	380	1	OPRK_HUMAN
22	334	15.5	388	1	SSR4_HUMAN
23	333.5	15.5	367	1	OPRK_MOUSE
24	333.5	15.5	367	1	OPRK_RAT
25	333.5	15.5	370	1	OPRK_PIG
26	333.5	15.5	428	1	SSR3_RAT
27	332.5	15.4	372	1	OPRD_HUMAN
28	331.5	15.4	395	1	TRFR_CHICK
29	331	15.4	372	1	GALS_RAT
30	330.5	15.3	428	1	SSR3_MOUSE
31	329.5	15.3	370	1	OPRK_HUMAN
32	328	15.2	380	1	OPRK_MOUSE
33	326.5	15.1	371	1	GALS_MOUSE

34	326.5	15.1	384	1	SSR4_RAT
35	323.5	15.0	370	1	GALT_RAT
36	321	14.9	384	1	SSR4_MOUSE
37	320.5	14.9	372	1	OPRD_RAT
38	320.5	14.9	398	1	TRFR_HUMAN
39	320	14.8	519	1	TLR2_DROME
40	319.5	14.8	368	1	GALT_HUMAN
41	319	14.8	372	1	OPRD_MOUSE
42	319	14.8	453	1	CKKR_XENLA
43	318.5	14.8	387	1	GALS_HUMAN
44	318.5	14.8	398	1	TRFR_BOVIN
45	318	14.7	353	1	AFU_XENLA

P30937 rattus norv
O88626 rattus norv
P49660 mus musculu
P33533 rattus norv
P34981 homo sapien
P30975 drosophila
O60755 homo sapien
P32300 mus musculu
P70031 xenopus lae
O43603 homo sapien
O46639 bos taurus
P79960 xenopus lae

ALIGNMENTS

RESULT 1
MTLR_HUMAN
ID MTLR_HUMAN STANDARD; PRT; 412 AA.
AC O43193;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Motilin receptor (G protein-coupled receptor GPR38).
GN GPR38 OR MTLR1 OR MTLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=98110578; PubMed=9441746;
RA McKee K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,
RA Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;
RT "Cloning and characterization of two human G protein-coupled receptor
genes (GPR38 and GPR39) related to the growth hormone secretagogue
and neurotensin receptors.";
RL Genomics 46:426-434 (1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=93116084; PubMed=10381885;
RA Feighner S.D., Tan C.P., McKee K.K., Palyha O.C., Hreniuk D.L.,
RA Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri M.A.,
RA Nargund R., Bakshi R., Abramovitz M., Stocco R., Kargman S.,
RA O'Neill G., van Der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G.,
RA Howard A.D.;
RT "Receptor for motilin identified in the human gastrointestinal
system.";
RL Science 284:2184-2188 (1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX Wall M.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBDJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE=21219832; PubMed=11322507;
RA Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D.,
RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.;
RT "Growth hormone secretagogue receptor family members and ligands.";
RL Endocrine 14:9-14 (2001).
CC -!- FUNCTION: Receptor for motilin.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=O43193-1; Sequence=Displayed;
CC Name=B;
CC IsoId=O43193-2; Sequence=VSP_001894;
CC -!- TISSUE SPECIFICITY: Expressed only in thyroid, stomach, and bone
marrow.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; AF034632; AAC26081.1; -;
 CC EMBL; AL137000; CAC19107.1; -;
 CC Genew; HGNC:4495; GPR38.
 CC MIM; 602885; -;
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
 CC GO; GO:0007586; P: digestion; TAS.
 CC GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; TAS.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR F1_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Alternative splicing.

CC FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 36 56
 CC FT DOMAIN 57 74 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 75 94
 CC FT DOMAIN 95 112 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 113 134
 CC FT DOMAIN 135 157
 CC FT TRANSMEM 158 178
 CC FT DOMAIN 179 246 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 247 270
 CC FT DOMAIN 271 298
 CC FT TRANSMEM 299 320
 CC FT DOMAIN 321 334
 CC FT TRANSMEM 335 358
 CC FT DOMAIN 359 412
 CC FT TRANSMEM 413 412
 CC FT BY SIMILARITY.
 CC FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT QLVLAFLICWLPFHVGRILIIYNTEDSRMMYFSQYFNIVAL
 CC QLVLSINPILYLNLSIKYRAAFKLLARKSRPRGFR
 CC SRDTAGEVAGTGTGVTYTSANVTMG -> RKWSRREG
 CC SKDACLOSAPGTACTLGLPLLAQLAPTPAPEPISIPAS
 CC TRRGSGSIYNLVALPRWQNLHKGFRFADVLVSL
 CC (in isoform B).
 CC /FTID=VSP_001894.
 CC SEQUENCE 412 AA; 45344 MW; CL3FF6165012DEF3 CRC64;

Query Match 99.7%; Score 2149; DB 1; Length 412;
 Best Local Similarity 99.8%; Pred. No. 6.3e-135;
 Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPALPCDERRCPPLGALVPTAVCLFVVGSGNVTV 60
 Db 1 MGSPWNGSDGPEGAREPPALPCDERRCPPLGALVPTAVCLFVVGSGNVTV 60
 QY 61 MLIGRVDMTNTNLYGMAVSDLLILGLPDLRLMSRPWWGPLLCRLSLVYGE 120
 Db 61 MLIGRVDMTNTNLYGMAVSDLLILGLPDLRLMSRPWWGPLLCRLSLVYGE 120
 QY 121 CTYATLLHMTALSVRYLAICRLPRLVTRVRVRLIAVLWAVALLSAGPLEFLVYGE 180
 Db 121 CTYATLLHMTALSVRYLAICRLPRLVTRVRVRLIAVLWAVALLSAGPLEFLVYGE 180
 QY 181 QDPGISVPLNGTARIASPLASSPLMLSRAPPSPGPGTAAALFSSRECRPSA 240
 Db 181 QDPGISVPLNGTARIASPLASSPLMLSRAPPSPGPGTAAALFSSRECRPSA 240
 QY 241 QLGLARVLMVWTTTAYFFPLCLISLYGLIGRLWSRRPLRGPASGRGHRQTVRL 300
 Db 241 QLGLARVLMVWTTTAYFFPLCLISLYGLIGRLWSRRPLRGPASGRGHRQTVRL 300

QY 301 LVVLAFLICWLPFHVGRILIIYNTEDSRMMYFSQYFNIVALQFLYLSASINPILNLSK 360
 Db 301 LVVLAFLICWLPFHVGRILIIYNTEDSRMMYFSQYFNIVALQFLYLSASINPILNLSK 360
 QY 361 KYRAAFAKLLARKSRPRGFRSRDTAGEVAGTGTGVTYTSANVTMG 412
 Db 361 KYRAAFAKLLARKSRPRGFRSRDTAGEVAGTGTGVTYTSANVTMG 412

RESULT 2

GHSR_PIG

ID GHSR_PIG STANDARD; PRT; 366 AA.
 AC Q95254; Q95255;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
 DE peptide receptor) (GHRP) (Ghrelin receptor).
 GN GHSR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RC STRAIN=Yorkshire; TISSUE=Pituitary;
 RX MEDLINE=96337998; PubMed=8688086;
 RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P.,
 RA Liberator P.A., Rosenblum C.I., Hreniuk M., Hreniuk D.L., Liu X.K.,
 RA Palaya O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu X.K.,
 RA McKee K.K., Pong S.-S., Chaur L.-Y., Elbrecht A., Dashkevich M.,
 RA Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,
 RA Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K.,
 RA Schaeffer J.M., Smith R.G., van der Ploeg L.H.R.;
 RA "A receptor in pituitary and hypothalamus that functions in growth
 hormone release.";
 RL Science 273:974-977(1996).
 CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
 CC Stimulates growth hormone secretion. Binds also other growth
 CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
 CC as well as non-peptide, low molecular weight secretagogues (e.g.
 CC 1-692,429, MK-0677, adenosine).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1A;
 CC IsoId=Q95254-1; Sequence=Displayed;
 CC Name=1B;
 CC IsoId=Q95254-2; Sequence=VSP_001918, VSP_001919;
 CC -!- TISSUE SPECIFICITY: Pituitary and hypothalamus.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----
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CC -----
 CC EMBL; U60178; AAC48630.1; -;
 CC EMBL; U60180; AAC48631.1; -;
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR F1_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Alternative splicing.
 CC FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 41 66
 CC FT CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 67

Query Match 39.7%; Score 855.5; DB 1; Length 364;
 Best Local Similarity 48.0%; Pred. No. 1.1e-49;
 Matches 184; Conservative 52; Mismatches 82; Indels 65; Gaps 11;

QY 5 WNGSDGPGAREP-----PWPALPPCD---ERRCSPPFLGALVPTAVCLCLFVVGVS 55
 Db 2 WNAT--PSEEPENVTLDWDASPGNDSLDPDELLFPAPLAGVATCAVLFVVGIS 59

QY 56 NVVTMLIGRYDMRTTNLYLGSMAVSDLLILGLPDLVLRWSRPMVGPGLCLSL 115
 Db 60 NLLTMLVSRFRRLRTTNLYLSSMAFSDLLFLCMLPDLVLRWQYRPNFGDLCKLFQ 119

QY 116 YVGEQTVATLHMTALSVERVLAICRPLRVLTTRRRVRLAVLMAVALLSAGPFLF 175
 Db 120 FVSECTATVLTITALSVERVYFAICPLRAKVVTKGRKLVILVAVAFCSAGPIFV 179

QY 176 LVGVEQDQGISVVGPGNGTARTASSPLASPLMLSRAPPPSPGPETAALAFSREC 235
 Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197

QY 236 RPS--PAQGLALRVMLVMTTAYFFLPFLCLSLYGLIGELWSSRRPLRGPAASG---RE 290
 Db 198 RATEFAVRSGLLTVMVWSSVFFFLVFLVCLTVLSLIGRKLW--RR--RGDAVVGSLRD 253

QY 291 RGHQTKRVLVVVLAIFIIICWLPVHGRYIINTEDS---RMMYFSQYFNIVALQLFVLS 347
 Db 254 QNHQTKVRLAVVVFAPFIIICWLPVHGRYLFKSPFPGSLFIAQISQYCNLVSPVLFVLS 313

QY 348 ASINPIYLNLSKKYRAAFKLL 370
 Db 314 AAINPIYLNMSKKYRVAVFKLL 336

RESULT 5
 GHSR MOUSE
 ID Q99P50; Q91Z82; STANDARD; PRT; 257 AA.
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing peptide receptor) (GHRP) (Ghrelin receptor) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-183 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RA Kacsch B.;
 RT "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA by rapid amplification of cDNA ends (RACE).";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 73-257 FROM N.A.
 RC STRAIN=129S3/SvImJ;
 RA Peng X., Frohman L.A., Kineman R.D.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6) as well as non-peptide, low molecular weight secretagogues (e.g. L-692,429, MK-0677, adenosine) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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CC EMBL; AY056474; AAL13336.1; --
 CC EMBL; AF332997; AAG61141.1; --
 DR InterPro; IPR000276; GPCR Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS02337; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS02622; G-PROTEIN RECP_F2_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 35
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 36 58
 FT DOMAIN 59 77
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 78 100
 FT DOMAIN 101 125
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 126 148
 FT DOMAIN 149 160
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 183
 FT DOMAIN 184 211
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 234
 FT DOMAIN 235 257
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 115 197
 FT BY SIMILARITY.
 FT CARBOHYD 13 13
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 26 26
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 187 187
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT NON TER 257 257
 SQ SEQUENCE 257 AA; 28743 MW; D6FA21EAB0E30791 CRC64;

Query Match 28.5%; Score 614; DB 1; Length 257;
 Best Local Similarity 45.1%; Pred. No. 6.4e-34;
 Matches 137; Conservative 39; Mismatches 66; Indels 62; Gaps 10;

QY 5 WNGSDGPGAREP-----PWPALPPCD---ERRCSPPFLGALVPTAVCLCLFVVGVS 55
 Db 2 WNAT--PSEEPENVTLDWDASPGNDSLDPDELLFPAPLAGVATCAVLFVVGIS 59

QY 56 NVVTMLIGRYDMRTTNLYLGSMAVSDLLILGLPDLVLRWSRPMVGPGLCLSL 115
 Db 60 NLLTMLVSRFRRLRTTNLYLSSMAFSDLLFLCMLPDLVLRWQYRPNFGDLCKLFQ 119

QY 116 YVGEQTVATLHMTALSVERVLAICRPLRVLTTRRRVRLAVLMAVALLSAGPFLF 175
 Db 120 FVSECTATVLTITALSVERVYFAICPLRAKVVTKGRKLVILVAVAFCSAGPIFV 179

QY 176 LVGVEQDQGISVVGPGNGTARTASSPLASPLMLSRAPPPSPGPETAALAFSREC 235
 Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197

QY 236 RPS--PAQGLALRVMLVMTTAYFFLPFLCLSLYGLIGELWSSRRPLRGPAASG---RE 290
 Db 198 RATEFAVRSGLLTVMVWSSVFFFLVFLVCLTVLSLIGRKLW--RR--RGDAVVGSLRD 253

QY 291 RGHQTKRVLVVVLAIFIIICWLPVHGRYIINTEDS---RMMYFSQYFNIVALQLFVLS 347
 Db 254 QNHQTKVRLAVVVFAPFIIICWLPVHGRYLFKSPFPGSLFIAQISQYCNLVSPVLFVLS 313

RESULT 6

NTRI1 RAT
 ID NTRI1 RAT
 AC P20789; STANDARD; PRT; 424 AA.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurotensin receptor type 1 (NTR-1) (High-affinity leucobastine-insensitive neurotensin receptor) (NTRH).
 DE NTSR1.
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
 RA MEDLINE=90297956; PubMed=1694443;
 RX Tanaka K., Masu M., Nakanishi S.;
 RT "Structure and functional expression of the cloned rat neurotensin
 receptor.";
 RL Neuron 4:847-854(1990).
 CC -1- FUNCTION: Receptor for the tridecapeptide neurotensin. It is
 associated with G proteins that activate a phosphatidylinositol-
 calcium second messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Highest to tachykinins receptors.
 DR PIR; JH0164; JH0164.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR003985; NTL_Receptor.
 DR InterPro; IPR003984; NTL_Receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01479; NEUROTENSINR.
 DR PRINTS; PR01480; NEUROTENSINR.
 DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_REC_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 64
 FT TRANSMEM 65 87
 FT DOMAIN 88 96
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 97 121
 FT DOMAIN 122 143
 FT TRANSMEM 144 165
 FT DOMAIN 166 188
 FT TRANSMEM 189 210
 FT DOMAIN 211 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 308
 FT TRANSMEM 309 330
 FT DOMAIN 331 348
 FT TRANSMEM 349 372
 FT DOMAIN 373 424
 FT CYTOPLASMIC (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 38 38
 FT CARBOHYD 42 42
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 142 225
 FT LIPID 388 388
 SQ SEQUENCE 424 AA; A9C2P7EAF8D9BCD3 CRC64;

Query Match 23.1%; Score 498; DB 1; Length 424;
 Best Local Similarity 32.9%; Pred. No. 4.9e-26;
 Matches 125; Conservative 58; Mismatches 111; Indels 86; Gaps 11;
 39 VPVTAVCLCLFVVGVSGNVVTVMLIGR---YRDMRTTNLYLGSMAVSDLLI-LLGLPFD 94
 65 VLVTAYIALFVVGTVGNSVATLARKKSLQSVTHVHLSLSDLLILLAMPVE 124
 95 LYR-LNRSRPWVGPCLLCRLSLVYGECTVATLHMTALSVRYLAICRPLRAVLVTR 153
 125 LYNFIWVHHPWAFGDAGCGRYFLRDCTVATNALVASLSVERLYLAICHPFKATLMSR 184
 154 RVKALLAVLWAVALLSAGPFLVGVQDQGISVWVGLNLTARIASPLASSPFLWLSRA 213
 185 RTKFKFSAIWLASALLAIPMLFTMGQLNRSQDGTGHPG-----GLVCTPIVDT----- 231
 214 PFPSPSPGPTAEAAALFSRECRPSPAQLGALRVMLVWVTTAYFFL-PFLCLSLYGLIGR 272
 232 -----ATVKVQVNTFMFSLFPLMVISLNVIVIAN 262
 273 ELWSSRRPLGPAASGR-----ERHQRQTKR-----VLLVWVLAFLII 309
 263 KLTWM---VHQAAEQGRVCTVGTGTHGLEHSTFNMTIEPGRVQALRHGVILRAVIAFVV 319
 310 CWLPFHVGRIIYINTEDSR---MMYFSQYFNIVVALQFLVLSASINPILNLSKKYRAA 365
 320 CWLPFHVVRMLMFCYISDEQWTTFLDFYHYFYMTNALFYVSSAINPILNLSVANFRQV 379

QY 366 AFKLLLA-----RKSRP 377
 DB 380 FLTLACLCPGWHRHRRKRP 399
 RESULT 7
 NTRL_MOUSE STANDARD; PRT; 424 AA.
 AC 088319;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurotensin receptor type 1 (NT-R-1).
 GN NTSR1 OR NTSR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Snider J., Sano H., Ohta M.;
 RT "Neurotensin receptor type 1.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for the tridecapeptide neurotensin. It is
 associated with G proteins that activate a phosphatidylinositol-
 calcium second messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Highest to tachykinins receptors.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB017027; BAA33013.1; -
 DR MGD; MGI:97386; Ntsr.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR003985; NTL_Receptor.
 DR InterPro; IPR003984; NTL_Receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01479; NEUROTENSINR.
 DR PRINTS; PR01480; NEUROTENSINR.
 DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_REC_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 64
 FT TRANSMEM 65 87
 FT DOMAIN 88 96
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 97 121
 FT DOMAIN 122 143
 FT TRANSMEM 144 165
 FT DOMAIN 166 188
 FT TRANSMEM 189 210
 FT DOMAIN 211 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 308
 FT TRANSMEM 309 330
 FT DOMAIN 331 348
 FT TRANSMEM 349 372
 FT DOMAIN 373 424
 FT CYTOPLASMIC (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 38 38
 FT CARBOHYD 42 42
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 211 224
 FT BY SIMILARITY.

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FT LIPID 388 388 S-palmitoyl cysteine (Potential).
SQ SEQUENCE 424 AA; 47216 MW; 8E9A723171A48711 CRC64;

Query Match 23.08; Score 495.5; DB 1; Length 424;
Best Local Similarity 33.6%; Pred. No. 6.6e-26;
Matches 127; Conservative 56; Mismatches 114; Indels 81; Gaps 12;

QY 39 PVPTAVCLCFVGVGSGNVVTVMILGR---YDRMRTTNNLYLGSMAVSDLLI-LLGLPFD 94
Db 64 VLVTAVYALFVVGTVGNSVTAFLARKKSLQSIQSVHYHGLSLASDLLILLAMPVE 123
QY 95 LYR-LWRSRWVFGPLICRLSLYVCECTVATLHNTALSVERVLAICRPLRARVLTTR 153
Db 124 LYNFIVWHFPAFGDAGCRGYFURDACTATALNVASLSVERVLAICHPFKATLMSRS 183
QY 154 RVRALIAVLMAVALLSGPFLFVGVQDPCGISVVGPLNGVARTASSPLPMLLSRA 213
Db 184 RTKFIISAIWLASALLAVPMLFTWGLQ-----NRS 213
QY 214 PPPSPGPGPETAEEAALFSRECPSPALQALRVMLVWTTAYFL-PFLCLSLILYGLIGR 272
Db 214 ADGQHPGG-----LVCTPT-VDTATVKVVIQVNTFMSLFPMLIISILNTVIAN 261
QY 273 EL-----KSSRPLRGPAASGR-----ERGHQTR-----VLAIVVLAFLICW 311
Db 262 KLTVMVHQABQGRGVCTVGTHTNSLEHSTFNMSIEBPGRVQALRHGVLRVLAIVAFVVCW 321
QY 312 LPFHVGRITIIYNTDSR-----MMVFQSVFNIVLQFLYLSASINPILYMLISKKYRAAF 367
Db 322 LPYHVRMLMFCYISDEQWTTFLDFYHYFVYMLTNALFVVSAINPILYMLNLSANFRQVFL 381
QY 368 KLLLA-----RKSRP 377
Db 382 STLACLCPGWRRRRKKRP 399

RESULT 8
ID NTRI HUMAN STANDARD; PRT; 418 AA.
AC P30989; Q9H4H1; Q9H4T5;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotensin receptor type 1 (NT-R1) (High-affinity levo-cabastine-
DE insensitive neurotensin receptor) (NTRH).
GN NTR1 OR NTRR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93154505; PubMed=8381365;
RA Vita N., Laurent P., Lefort S., Chalou P., Dumont X., Kaghad M.,
RA Gully D., le Fur G., Ferrara S., Caput D.;
RT "Cloning and expression of a complementary DNA encoding a high
RT affinity human neurotensin receptor.";
RL FEBS Lett. 317:139-142(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

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RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslaio M.H., Leverha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLeod J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.B., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RA "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- FUNCTION: Receptor for the tridecapeptide neurotensin. It is
CC associated with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Highest to tachykinins receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: X70070; CAA49675.1; -
EMBL: AL357033; CAC14923.1; -
EMBL: AL035669; CAC12747.1; -
PIR: S29506; S29506.
HSSP: P02699; 1F88.
Genew: HGNC:8039; NTSR1.
MIM: 162651.
GO: GO:0005783; C:endoplasmic reticulum; TAS.
GO: GO:0005794; C:Golgi apparatus; TAS.
GO: GO:0005887; C:integral to plasma membrane; TAS.
GO: GO:0004930; P:G-protein coupled receptor activity; TAS.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
GO: GO:0007268; P:synaptic transmission; TAS.
InterPro: IPR000276; GPCR_Rhodops.
InterPro: IPR003985; Ntr_receptor.
InterPro: IPR003984; Ntr_receptor.
Pfam: PF00001; 7tm.1; 1.
PRINTS: PR00237; GPCRHOODPSN.
PRINTS: PR01479; NEUROTENSINR.
PRINTS: PR01480; NEUROTENSINR.
PROSITE: PS00237; G_PROTEIN_REC_F1_1; 1.
PROSITE: PS0262; G_PROTEIN_REC_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 63
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 64 86
FT DOMAIN 87 95
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 120
FT DOMAIN 121 142
FT TRANSMEM 143 164
FT DOMAIN 165 187
FT TRANSMEM 188 209
FT DOMAIN 210 234
FT TRANSMEM 235 259
FT DOMAIN 260 303
FT TRANSMEM 304 325
FT DOMAIN 326 343
FT TRANSMEM 344 367
FT DOMAIN 368 418
FT CARBOHYD 4
FT CARBOHYD 37
FT CARBOHYD 41
FT DISULFID 141

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FT  LIPID      383      383      S-palmitoyl cysteine (Potential).
FT  CONFLICT  200      200      T -> A (IN REF. 2).
SQ  SEQUENCE  418 AA;  46288 MW;  BBBDIEEC2BE6E390 CRC64;

Query Match      22.8%; Score 491; DB 1; Length 418;
Best Local Similarity 32.8%; Pred. No. 1.3e-25;
Matches 125; Conservative 62; Mismatches 118; Indels 76; Gaps 13;

QY  39  VPVTAVCLCLFVGVSGNVTVMLIGR---VRDMRTTNLYLGMVSDLL-IILGLPFD 94
DQ  64  VLVTAVALFVGVGVGNVTVAFTIARKKSLQSLQSTVHYHGLSLASDLLTLILAMPVE 123
QY  95  LYR-LWRSPVWFGPLCLSLYVGGCTATLHMTALSVERYLAICRPLRARVLTTR 153
DQ  124  LYNFIWVHPHAFDAGRGYFFDADCTATYALNVAISLVERYLAICHPFKATILMSRS 183
QY  154  RVRALIAVLNVALLSAGPFLFLVGEQDPGISVVVGLNGTARIASSPLSSPFLWLSRA 213
DQ  184  RTKKFISAIWLASALLTVPMFLTMG-EQN----- 211
QY  214  PPPPPSPGPTAEAAALPSRRCRSPALQALRVMLWTT-AYFELPCLLSILYGLIGR 272
DQ  212  -----RADGOGHAGGLVCTPT-IHTATVKVIVQVNTFMSEIFPMVIVSLNTIAN 261
QY  273  ELWSSRRPL--RGPAAS-----GRGRGHROTQRVLLVVVLAFTIICWLPFHV 316
DQ  262  KLTVMVQAARQGVCTVGGHSTFSEMAIEPGRVQALRHGVRLRAVIAFVWMLPHV 321
QY  317  GRIIYINTEDSR---MMY-FQYFNIVALQFYLSASINPLYNLSKKYR-----AA 365
DQ  322  RRLMFCVISDQWTFPLDFHYFYMTVNLVYVSSSTINPLYNLVSANFRHIFLATLAC 381
QY  366  AFKLLIARKSPRGPHRSRDT 386
DQ  392  LCPVWRRRRKRP-AFSRXADS 401

RESULT 9
CAPR DROME STANDARD; PRT; 477 AA.
AC  Q8ITC7; Q8VPI5;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Neuropeptides capa receptor (Cap2b receptor).
GN  CAPAR OR CG14575
OS  Drosophila melanogaster (Fruit fly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7227;
RN  [1]
RC  SEQUENCE FROM N.A., AND FUNCTION.
RX  STRAIN=Canton-S;
RX  MEDLINE=22177201; PubMed=12177421;
RA  Park Y., Kim Y.J., Adams M.E.;
RT  "Identification of G protein-coupled receptors for Drosophila PRXamide
RT  peptides, CCAP, co-receptor, and AKH supports a theory of
RT  ligand-receptor coevolution."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:11423-11428(2002).
RN  [2]
RC  SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
RP  STAGE.
RX  MEDLINE=22347021; PubMed=12459185;
RA  Iversen A., Gazzamali G., Williamson M., Hauser F.,
RA  Grimelikhuijzen C.J.P.;
RT  "Molecular cloning and functional expression of a Drosophila receptor
RT  for the neuropeptides capa-1 and -2."
RL  Biochem. Biophys. Res. Commun. 299:628-633(2002).
RN  [3]
RC  SEQUENCE FROM N.A.
RP  STRAIN=Berkley;
RX  MEDLINE=20196006; PubMed=10731132;

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RA  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA  Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA  Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA  Borokova D., Botchan M.R., Bouch J., Brokstein P., Brottier P.,
RA  Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M.,
RA  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA  Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA  Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA  Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA  Lasako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA  Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,
RA  Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA  Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA  Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA  Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster."
RL  Science 287:2185-2195(2000).
RN  [4]
RP  REVISIONS.
RX  MEDLINE=22426069; PubMed=12537572;
RA  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA  Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA  Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA  Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA  Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA  Lewis S.E.;
RT  "Annotation of the Drosophila melanogaster euchromatic genome: a
RT  systematic review."
RL  Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
CC  -!- FUNCTION: Acts as a receptor for the neuropeptides CAP-1 and CAP-
CC  2, but not CAP-3. Probably a component of signal transduction
CC  pathway that leads to Malpighian tubule fluid secretion in
CC  response to these ligands.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC  -!- TISSUE SPECIFICITY: In adults, expression in thorax and/or
CC  abdomen.
CC  -!- DEVELOPMENTAL STAGE: Expressed weakly in 16-24 hour embryos and
CC  second instar larvae and strongly in first and third instar larvae
CC  and adults.
CC  -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC  -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC  gene model prediction.
CC  -----
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CC  or send an email to license@sib-sib.ch).
CC  -----

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DR EMBL; AF522193; AANI0046.1; -
DR EMBL; AF505865; AAO20968.1; -
DR EMBL; AB003594; AAF51746.2; ALT_SEQ.
DR FlyBase; FBgn0037100; capar.
DR GO; GO:0016021; C: integral to membrane; NAS.
DR GO; GO:0004930; F: G-protein coupled receptor activity; IDA.
DR GO; GO:0008188; F: neuropeptide receptor activity; IDA.
DR GO; GO:0007589; P: fluid secretion; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
DR Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 72 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 73 93
FT DOMAIN 94 109
FT TRANSMEM 110 130
FT DOMAIN 131 145
FT TRANSMEM 146 166
FT DOMAIN 167 189
FT TRANSMEM 190 210
FT DOMAIN 211 237
FT TRANSMEM 238 258
FT DOMAIN 259 295
FT TRANSMEM 296 316
FT DOMAIN 317 335
FT TRANSMEM 336 356
FT DOMAIN 357 477
FT DISULFID 142 228
FT CARBOHYD 2 2
FT CARBOHYD 13 13
FT SEQUENCE 477 AA; 54004 MW; 34FBE13F301A9F4D CRC64;

Query Match      20.9%; Score 451; DB 1; Length 477;
Best Local Similarity 29.7%; Pred. No. 6.3e-23;
Matches 117; Conservative 69; Mismatches 135; Indels 74; Gaps 11;

QY 8 SDGPEGAREPPWALPPCDERRCSP-----FPLGALVPTAVCLFLFVVGVSG 55
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 56 NVVTVMIGRYDMRTTNYLIGSMVSDLLILL-GLPFDLYLWRSRPMVFGPLCLRLS 114
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 86 NLLVCVILRHSAHMTATNYLFLSLAVSDLLYLLGLPFEVLYWQYDPLFGMPFCKIR 145
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 115 LVYGECTATLHMTALSVERVLAICRPARAVLVTRRRVRALIAVLNAVALLSAGPFL 174
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 146 AFISEACTYVSVPTIVAFSGMERELAICHPHLHYAMVGFKRAIRITALTIVTSFSAIPF- 204
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 FLVGVQDPGISVVVGLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRE 234
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 205 -----GLLSDIQVNLPLDHS-----RIESAF----- 227
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 CRPSPAQLGALRYMLVMTTAYFFLPFLCLSLYGLICRELWSSRRPLRG--PAASGRERG 292
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 228 CSMSPKIVNEIPVFEVSFCIFFVPIMLIILLYGRMGAKIRSTNQKLGVOQTNRETR 287
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 293 HRQTK-----RVLLVTVLAFILCWLFPHVGRITIIYNTESRMVYFQYENI-----VAL 341
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 288 NSQMRKKTIVIRMLAAVVITFFVCVFFPHLQRLFLYAKN-----MDNYLDINEALFSIAG 342
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 342 QLFYLSASINPILYNLISKYRAAFAKLLIARKS 375
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 343 FAYVSVCTNPVIVSVMSRRYR-VARELLCGKA 375
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
ID NTR2 HUMAN STANDARD; PRT; 410 AA.
AC Q95655; Q8TBH6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotensin receptor type 2 (NT-R-2) (Levocabastine-sensitive
DE Neurotensin receptor) (NTR2 receptor).
GN NTR2.
OS Homo sapiens (Human).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99086919; PubMed=9851594;
RX Vita N., Oury-Donat F., Chalon P., Guillemot M., Kaghad M., Bachy A.,
RA Thurneyssen S., Garcia S., Poinot-Chazel C., Casellas P., Keane P.,
RA Le Fur G., Maffrand J.-P., Shoubrie P., Caput D., Ferrara P.,
RT "Neurotensin is an antagonist of the human neurotensin NT2 receptor
expressed in Chinese hamster ovary cells.";
Eur. J. Pharmacol. 360:265-272(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesfeld J.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.E., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for the tridecapeptide neurotensin. It is
associated with G proteins that activate a phosphatidylinositol-
calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Highest to tachykinins receptors.
-----
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EMBL; Y10148; CAA71233.1; -
DR EMBL; BC022501; AAH22501.1; -
DR GenBank; HGNC:8040; NTR2.
DR MIM; 605538; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
DR GO; GO:0007166; P: cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0007600; P: sensory perception; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR003986; NT2_receptor.
DR InterPro; IPR003984; NT_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR01479; NEUROTENSINR.
DR PRINTS; PR01481; NEUROTENSINR.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.

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QY 190 GLNGTARIASSPPLWLSRAP-PPSPSGFETAAALRSRCRPPAQI---GAL 245
 Db 180 -----MERADGEPEPAS-----RVCTVLVSRRASSTFQVKGAGLL 215
 QY 246 RVMLWVTTA-----YFFLPFLC-----LSIL--YGLIGRELWSSRRPL 281
 Db 216 RSLFWELTALINGITVNHVLVALSQVPSASAQVNSIPSRLELSEGLGFIITWKYLSL 275
 QY 282 RGAASGRBRGHQTK-----RVLLVVLAFIICWLPFHVGRIIYINTED-----SRMMY 331
 Db 276 GVOASLVRHKDAQIRSLQHSQAQLRAIVAVVVICWLPYHARLMYCIYIPDDGWTDELYD 335
 QY 332 FSOYFNVALQLFVLSINPILYNLISKYRAAPKLLILARKSRPRGPHRS 383
 Db 336 FYHYFYVNTLFSVAVTPVLYNAVSSFR-----KLFLESLSLSCGBOQS 383

RESULT 12

NTR2 RAT
 ID NTR2 RAT STANDARD; PRT; 416 AA.
 AC Q63384;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Neurotensin receptor type 2 (NT-R-2) (High-affinity levocabastine-sensitive neurotensin receptor).
 GN NTR2 OR NTR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=96228041; PubMed=8647296;
 RA Chalon P., Vita N., Kaghad M., Guillemont M., Bonin J.,
 RA Delpech B., le Fur G., Ferrara P., Caput D.;
 RT "Molecular cloning of a levocabastine-sensitive neurotensin binding site";
 RL FEBS Lett. 386:91-94(1996).
 CC -!- FUNCTION: Receptor for the tridecapeptide neurotensin. It is associated with G proteins that activate a phosphatidylinositol-calcium second messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Abundant in cortex and hypothalamus, and lower levels seen in the heart and intestine.
 CC -!- DEVELOPMENTAL STAGE: Expressed maximally in 7-day-old brain and expression decreases progressively until adulthood (35-day-old brain).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Highest to tachykinins receptors.

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 CC -----
 CC EMBL; X97121; CAA65787.1; -;
 CC PIR; S68822; S68822.
 CC InterPro; IPR000276; GPCR_Rhodop.
 CC InterPro; IPR003986; NT2_receptor.
 CC InterPro; IPR003984; NT_receptor.
 CC Pfam; PF00001; 7tm1.1;
 CC PRINTS; PR00237; GPCR_RHOOPSN.
 CC PRINTS; PR01479; NEUROTENSINR.
 CC PRINTS; PR01481; NEUROTENSINR.
 CC PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Lipoprotein; Palmitate.

FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 33 55 1 (POTENTIAL).
 FT DOMAIN 56 64 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 65 87 2 (POTENTIAL).
 FT DOMAIN 88 109 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 110 131 3 (POTENTIAL).
 FT DOMAIN 132 154 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 155 176 4 (POTENTIAL).
 FT DOMAIN 177 216 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 217 237 5 (POTENTIAL).
 FT DOMAIN 238 297 6 (POTENTIAL).
 FT TRANSMEM 298 318 7 (POTENTIAL).
 FT DOMAIN 319 337 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 338 358 7 (POTENTIAL).
 FT DOMAIN 359 416 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 108 194 BY SIMILARITY.
 FT LIPID 377 377 S-palmitoyl cysteine (Potential).
 SQ SEQUENCE 416 AA; 46265 MW; 127FC5F5CB6FE208 CRC64;
 Query Match 18.6%; Score 401; DB 1; Length 416;
 Best Local Similarity 29.4%; Pred. No. 1.1e-19;
 Matches 122; Conservative 68; Mismatches 145; Indels 80; Gaps 13;
 QY 18 PWPALP-----PCDERCRSPPLGALVPVAVCLCLFVVGVSGNVVTVMLIGRYDMRT 71
 Db 6 PWPPEPSAGLSLEARLGVDTRLWAKVLTALYSLIFAFGTAGNALSVHVLKARAGR 65
 QY 72 -TNNLYGSMAYSDLLILL-GLPFDLYR-LWRSRPWVFGPCLLCRLSLVYVGGCTVATLLH 128
 Db 66 GLRYHVLSLALSALLLVSNPMLYFVWHPVWFGDLGCRGYVYFRELCAVATVLS 125
 QY 129 MTALSVERYLAIQRLPARVLVTRRVRALIAVLNAVALLSAGPFLFLVGV----- 179
 Db 126 VASLSAERCLAVCQPLRAERLTPRTRELLSLVWVASLGLALPMAVINGQKHEVESADG 185
 QY 180 EODPGISVVVGLNGTARIA-----SSPLASSPPLWLSRAPPPSPSGPETAEAA 228
 Db 186 EEPASRVCTVLVSRAVLQVFTQVNVLSFAULPALTAEF-----NGITVNHLM 234
 QY 229 ALFSRECRPSAQLGALRWLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPILRGPAASG 288
 Db 235 ALYS-QVPSASQVSSIPSRLELSE-----EGLGFTWRTLSLGVQASLV 281
 QY 289 REGRHRTK-----RVLLVVLAFIICWLPFHVGRIIYINTED-----SRMYFSQYFNI 338
 Db 282 RHKDAQIRSLQHSQAQLRAIVAVVVICWLPYHARLMYCIYIPDDGWTNELYDFHYFYM 341
 QY 339 VALQLFYLASINPILYNLISKYRAAPKLLILARKSRPRGPHRSRDTAGEVAGD 393
 Db 342 VTNTLFYVSSAVTPILYNNAVSSFR-----KLF-----ESLGSLSGGE 379

RESULT 13

SSRS MOUSE
 ID SSRS MOUSE STANDARD; PRT; 362 AA.
 AC Q08958; Q08998;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Somatostatin receptor type 5 (SSSR).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ; TISSUE=Liver;
 RX MEDLINE=97444289; PubMed=9300821;
 RA Lublin A.L., Diehl N.L., Hochgeschwender U.;
 RT "Isolation and characterization of the gene encoding the type 5 mouse (Mus musculus) somatostatin receptor (msst5).";
 RT Gene 195:63-66(1997).
 RL


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DR EMBL; X74828; CAA52825.1; -.
DR PIR; I57940; I57940.
DR HSP; P02699; I588.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G PROTEIN RECF F1.1; 1.
DR PROSITE; PS0262; G PROTEIN RECF F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 63 1 (POTENTIAL).
FT DOMAIN 64 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 99 2 (POTENTIAL).
FT DOMAIN 100 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 155 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 156 176 4 (POTENTIAL).
FT DOMAIN 177 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 221 5 (POTENTIAL).
FT DOMAIN 222 247 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 248 273 6 (POTENTIAL).
FT DOMAIN 274 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 308 7 (POTENTIAL).
FT DOMAIN 309 363 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 23 23 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 110 185 BY SIMILARITY.
FT LIPID 320 320 S-palmitoyl cysteine (Potential).
SQ SEQUENCE 363 AA; 39971 MW; 48D4512960613B4A CRC64;

Query Match
Best Local Similarity 16.6%; Score 358; DB 1; Length 363;
Matches 110; Conservative 27.3%; Pred. No. 6.6e-17;
Indels 84; Gaps 12;

QY 5 WNGSDGEGAREPPWALPPCDERRCSPFPLGA---LVPVTAVCLCLFVVGVSGNVVTVM 61
DB 12 WNASAASSGNH--WSLVG-----SASPMGARAVLPVLYLLVC--TVGLSGNTLIVY 60
QY 62 LIGRYDRMTTNLYLGMAVSLLILLGLLPDLRLWRSPWVFGPLLCRLSLYVGE 121
DB 61 VLVRHAKMTVTNVYTLNLAADVLFMLGLPFLATQNAVVSYPFGSFLCRLVMTLDGIN 120
QY 122 TYATLLHMTALSVERYLAI CRPLRARVLVTRRVRALIAVLMAVALLSAGPFLVGVGE 181
DB 121 QFTSIFCLMWSVDRLAVVHPARSARWRPRVAKASAAVWVFLMSLPLLVFADVQE 180
QY 182 DPGISVVGUNGTAIASSPLASSPPLWLSRAPPPSPGPETAATAAALFSRECRPSPAQ 241
DB 181 G-----WGTCNLS-----W-----PEPVG 194
QY 242 LGLALRVMLVTTAYFPLPFLCISLYGLI-----GRELWSSRRPLRGPAASGRGRGHR 294
DB 195 LKGAARITYTVLGVFGPLLVICLVLLIVVKAAGMRVGSRR-----RRRSEP 244
QY 295 QTKRVLVVVLAFLICWLPVHVGRIIYN-TEDSRMMYFQYENIVALQLFYLASINPI 353
DB 245 KVTMRVVVVVLFVGCWLPFFIVNVINLAFTLPEETSAGLYFFVVLS--YANSCANPL 302
QY 354 LYNLISKYTRAAAFKULLARKSRPRGHRSDRTAGVAGDTG 396
DB 303 LYGFLSDNFRQSPKVKVLCRLR---RGYGMEDADAIEPRPDKSG 341

RESULT 15
SSR3_HUMAN
ID SSR3_HUMAN STANDARD; PRT; 418 AA.
AC P32745;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Somatostatin receptor type 3 (SS3R) (SSR-28).

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GN

OS

OC

OC

OC

OX

RN

RP

RX

RA

RA

RT

RT

RL

RN

RP

RX

RA

RA

RT

RT

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RA

RT

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RN

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Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

SEQUENCE FROM N.A.

MEDLINE=93149123; PubMed=1337145;

Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.,

Seino M., Seino Y., Bell G.I., Seino S.;

"Somatostatin receptors, an expanding gene family: cloning and

functional characterization of human SS3R, a protein coupled to

adenylyl cyclase.";

Mol. Endocrinol. 6:2136-2142(1992).

[2]

SEQUENCE FROM N.A.

MEDLINE=93238970; PubMed=8097479;

Cernese J.D., Demchishyn L.L., Seeman P., van Tol H.H.M.,

Srikant C.B., Kent G., Patel Y.C., Niznik H.B.;

"A human somatostatin receptor (SS3R), located on chromosome 22,

displays preferential affinity for somatostatin-14 like peptides.";

FEBS Lett. 321:279-284(1993).

[3]

SEQUENCE FROM N.A.

Kopatz S.A., Atonstam R.S., Sharma S.V.;

"cDNA clones of human proteins involved in signal transduction

sequenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

[4]

SEQUENCE FROM N.A.

MEDLINE=20057165; PubMed=10591208;

Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,

Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,

Baggaley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,

Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,

Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,

Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,

Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,

Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,

Hunt S.E., Jones M.C., Kersey J., Kimberley A.M., King A.,

Laird G.K., Langford C.P., Leversha M.A., Lloyd C., Lloyd D.M.,

Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,

McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,

Odeh C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,

Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,

Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,

Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,

Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,

Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,

Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,

Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,

Lewis J., Lewis S., Lin S.-P., Loh P., Mala J.E., Nguyen T., Pan H.,

Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,

Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,

Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,

Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,

Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,

Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing J.,

Schett P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson T.,

Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,

Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,

Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,

Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,

Feyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,

O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,

Khan A.S., Lane L., Tilahun Y., Wright H.;

"The DNA sequence of human chromosome 22.";


```

RL Nature 402:489-495 (1999).
CC -!- FUNCTION: Receptor for somatostatins-14 and -28. This receptor is
CC coupled via pertussis toxin sensitive G proteins to inhibition of
CC adenylyl cyclase.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Brain, pituitary and pancreas.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M96738; AAB60592.1; -
CC EMBL; Z82188; CAB45263.1; -
CC EMBL; AY322541; AAB84354.1; -
CC PIR; A46226; A46226.
CC HSP; P34996; 1DDO.
CC Genew; HGNC:11332; SSTR3.
CC MIM; 182453; -
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004994; F:somatostatin receptor activity; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
CC GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Polymorphism
KW DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 69 1 (POTENTIAL).
FT DOMAIN 70 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 101 2 (POTENTIAL).
FT DOMAIN 102 116 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 117 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 231 5 (POTENTIAL).
FT DOMAIN 232 257 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 258 279 6 (POTENTIAL).
FT DOMAIN 280 293 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 294 316 7 (POTENTIAL).
FT DOMAIN 317 418 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 116 191 BY SIMILARITY.
FT DOMAIN 346 360 GLU-RICH (ACIDIC).
FT VARIANT 411 411 S->T (in dbSNP:229568).
FT /FTID=VAR_011853.
SQ SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;

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Query Match 16.5%; Score 356.5; DB 1; Length 418;
Best Local Similarity 26.9%; Pred. No. 9,5e-17;
Matches 101; Conservative 63; Mismatches 146; Indels 65; Gaps 10;

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QY 11 PEGAREPFWPALPPCDERRCSPFPL-----GALVPTAVCLCLFVYGVSGNVVTVMFLGR 65
DQ ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 15 PENA-SSAWPPDATTGNVSGAPSPAGLAVSGVILPLVYVVC--VVGGLGNSLVYVVL 71
QY 66 YRDMETTNLYGMAVSDLLILGLPDLVLRWSRPVWFGPLLCRLSLYVGECTVAT 125
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 72 HTAGSPVTNVILNALADELFMLGLPF-LAAQNALSYWPFGLMCRVMAVDGINQFTS 130
QY 126 LLHMTALSVRYLAICRLRLARVLVTRRRRVALLIWLAVALLSAGPFLFLVGVQDDPGI 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 131 IFCLTWSVDRLAVVHETRSARMTAPVARTVSAVWVAVVVLPVTVFSGV----- 184
QY 186 SVVPGNLGTARIASSPLASSPPLMLSRAPPSPSPGPPTABAAALFSRECR---PSPAQL 242
Db 185 -----PRGMST-----CHMQWPEPAAA 201
QY 243 GALRVMLWVTTAYFPLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRGHROTKEVLLV 302
Db 202 WRAGFIITTAALGFPGPLLVICLCYLLVVVRSGRRVWAPSCORRRSRRVTRMVA 261
QY 303 VVLAFTICWLPFHVGRITTYINTE-DSRMMYFSQYFNIVALQVLYLSASINPLYNLSKK 361
Db 262 VVALFVLCWMPFFVYLVNIVNVVCPLEPEAFGLYFLVALP--YANSCANPLYGFLSYR 319
QY 362 YRAAFKLLLLARKSR 376
Db 320 FK-QGFRVLLRPSR 333

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Search completed: July 4, 2004, 03:07:50
Job time : 20 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 02:04:17 ; Search time 73 Seconds
(without alignments)
1780.733 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPWNGSDPEGAREPPWP.....DTGSDTVGYTETSANVKTMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	901	41.8	363	13	Q93413 spherooides
2	855.5	39.7	364	11	Q8BWX8 mus musculus
3	849	39.4	347	13	Q7ZT14 gallus gall
4	845	39.2	374	13	Q93412 spherooides
5	819.5	38.0	366	6	Q8MH25 ovis aries
6	753	34.9	331	13	Q7ZZJ9 gallus gall
7	637	29.5	267	13	Q7ZZJ8 gallus gall
8	602	27.9	559	13	Q93414 spherooides
9	486.5	22.6	426	4	Q8NE20 Q9ne20 homo sapien
10	484.5	22.5	426	4	Q9HB89 Q9hb89 homo sapien
11	475.5	22.1	395	11	Q91Z76 mus musculus
12	475.5	22.1	395	11	Q8BZ39 mus musculus
13	475	22.0	415	4	Q96AM5 Q96am5 homo sapien
14	474	22.0	415	4	Q9GZQ4 Q9gzq4 homo sapien
15	472.5	21.9	395	11	Q9J1B1 Q9jjb1 rattus norv
16	470.5	21.8	395	11	Q9ESQ4 Q9esq4 rattus norv

17	456.5	21.2	405	11	O55040
18	434	20.1	418	5	O17239
19	430	19.9	428	5	Q9VFN4 Q9vfn4 caenorhabdi
20	430	19.9	430	5	Q8ITC9 Q8itc9 drosophila
21	414	19.2	595	5	Q8ITD0 Q8itd0 drosophila
22	414	19.2	593	5	Q9VFW6 Q9vfw6 drosophila
23	410	19.0	402	11	Q9J1B2 Q9jjb2 rattus norv
24	405	18.8	412	11	Q9J1J5 Q9jjj5 rattus norv
25	396.5	18.4	416	11	Q8VIF5 Q8vif5 mus musculu
26	395.5	18.3	416	11	Q920Q5 Q920q5 mus musculu
27	386	17.9	660	5	Q9VFW5 Q9vfw5 drosophila
28	384	17.8	658	5	Q8ITD1 Q8itd1 drosophila
29	378	17.5	378	5	Q18701 Q18701 caenorhabdi
30	376	17.4	123	11	Q80UB2 Q80ub2 mus musculu
31	370.5	17.2	461	5	Q86RK9 Q86rk9 drosophila
32	369.5	17.1	385	11	Q9JK40 Q9jk40 mus musculu
33	368.5	17.1	461	5	Q86062 Q86c62 drosophila
34	368.5	17.1	471	5	Q86RL0 Q86rl0 drosophila
35	368.5	17.1	471	5	Q86C63 Q86c63 drosophila
36	357.5	16.6	377	13	Q7T2S9 Q7t2s9 carassius a
37	356.5	16.5	385	4	Q86YF2 Q86yf2 homo sapien
38	356	16.5	452	13	Q7T2S8 Q7t2s8 carassius a
39	355.5	16.5	401	13	Q8JFZ6 Q8jفز6 xenopus lae
40	353.5	16.4	401	13	Q9DDR0 Q9ddr0 xenopus lae
41	349	16.2	477	13	Q8J1D5 Q8j1d5 carassius a
42	348.5	16.2	367	6	Q8MI04 Q8mi04 ovis aries
43	344	16.0	440	13	Q7T298 Q7t298 brachydanio
44	340.5	15.8	370	13	Q8UWL5 Q8uwl5 fugu rubrip
45	339	15.7	145	6	O97914 O97914 ovis aries

ALIGNMENTS

RESULT 1

O93413 ID O93413 PRELIMINARY; PRT; 363 AA.
AC O93413
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orphan G protein-coupled receptor.
OS Spherooides nephelus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Spherooides.
OX NCBI_TaxID=39110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20032336; PubMed=10628755;
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,
RA Patchett A.A., Howard A.D., Smith R.G.;
RT "Ligand activation domain of human orphan growth hormone (GH)
secretagogue receptor (GHS-R) conserved from pufferfish to humans.";
RL Mol. Endocrinol. 14:160-169(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF082210; AAC33473.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1_2; 1.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1_3; 1.
KW G-protein coupled receptor; Transmembrane.
SQ SEQUENCE 363 AA; 41324 MW; 74518BD9CD310991 CRC64;
Query Match 41.8%; Score 901; DB 13; Length 363;

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Best Local Similarity 50.3%; Pred. No. 2e-67; Indels 44; Gaps 5;
Matches 179; Conservative 56; Mismatches 77;

QY 31 SPFFLGALVPVAVCLCLFVVGSGNVVTVMLIGRYDMRTTNLYLGSMAVSDLLILIG 90
Db 31 SLFPASTLIPVTVICILFVVGVTGNTWILLIQYFKDMKTYTNLYLSMAVSDLVIFLC 90
QY 91 LPFDLYLRWRSPVWFGPLLRLSLSYVGEQCTYATLLHMTALSVERYLAICRPLARVLV 150
Db 91 LPFDLYLRWKVWPMFGEAVCRLYHIYIEGCTSATILHITALSIBERYLAISFPPLRSKUMV 150
QY 151 TRRRVRLIALIWMALVALLSAGPFLVGVQDPGIVSVVPGNGTARIASSPLASSPPLWL 210
Db 151 TRRRVQYIILALMCPALVSAAPTLFVGVQDPGIVSVVPGNGTARIASSPLASSPPLWL 210
QY 211 SRAPPPSPSPGTAETAAALFSRECRPSPAQL--GALRVMLWVTVTAYFFLPCLISILYG 268
Db 211 SRAPPPSPSPGTAETAAALFSRECRPSPAQL--GALRVMLWVTVTAYFFLPCLISILYG 268
QY 196 ---HPDYNTG-----QCKHTGYAIISSGQLHIMIWVSTYFPCWMLCLFLYG 229
Db 196 ---HPDYNTG-----QCKHTGYAIISSGQLHIMIWVSTYFPCWMLCLFLYG 229
QY 269 LIGRELSSRPLRQPAASGRGHRQTKRVLLVVLAFIICWLPFHVGRYIYINTEDSR 328
Db 230 SIGCKLWKSNDLQGPCALARSRSRQTKRVLLVVLAFIICWLPFHVGRYIYINTEDSR 328
QY 329 NMYFQSYENIVALQFLYSASINPILYNLSKYRAAFKLLARKSRPRGFRHSR 384
Db 290 TAMLSQNFNMAWVLCYLSASINPVVYVNLMSKYRAAKRFLFHQ-RPKPAHRCQ 344

RESULT 2
QBMWX8 PRELIMINARY; PRT; 364 AA.
AC Q8BMX8:
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type 1 homolog.
GN GHSR OR C530020122RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=23254683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK049671; BAC33866.1; -.
DR MGD; MGI:2441906; Ghr.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
SQ SEQUENCE 364 AA; 40969 MW; 8F1214E58EF3B2E8 CRC64;

Query Match 39.7%; Score 855.5; DB 11; Length 364;
Best Local Similarity 48.0%; Pred. No. 1.3e-63;
Matches 184; Conservative 52; Mismatches 82; Indels 65; Gaps 11;

QY 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPFLGALVPVAVCLCLFVVGVS 55
Db 2 WNAAT--PSEEPENVTLDDWDASPGNDSLSDELPLFPAPLAGVATCATCVAFVVGISG 59
QY 56 NVVTVMLIGRYDMRTTNLYLGSMAVSDLLILIGLPFDLYLRWRSPVWFGPLLRLSL 115
Db 60 NLLTLMVVSFRRELRTTNLYLSSMAVSDLLILIGLPFDLYLRWRSPVWFGPLLRLSL 119
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QY 116 YVGEQCTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIALIWMALVALLSAGPFLF 175
Db 120 FVSESCYATVLTITALSVERYFAICFPLRAKVTVTKGRVKLVILVIWAVAFCSAGPIFV 179
QY 176 LVGVQDPGIVSVVPGNGTARIASSPLASSPPLWLSRAPPPSPGTAETAAALFSRE 235
Db 180 LVGVHE-----NGT-----DPRD-----TNEC 197
QY 236 RPS--PAQLGALRVMLWVTVTAYFFLPCLISILYGLIGRELSSRPLRGPASG---RE 290
Db 198 RATEFAVRSGLLTVWVSSVFFLPFVCLIVLSLGRKLM--RR--RGDAVGVSSLRD 253
QY 291 RGHQTKRVLLVVLAFIICWLPFHVGRYIYINTEDS---RMMYFQSYENIVALQFLYS 347
Db 254 QNHRQTKVMLAVVVFAPILCWLPFHVGRYLFSGFEPSGLEIAQISQYCNLVSVFLFYLS 313
QY 348 ASINPILYNLSKRYRAAFKLL 370
Db 314 AAIPILYNIMSKKRYVAVFKLL 336

RESULT 3
Q7ZT14 PRELIMINARY; PRT; 347 AA.
AC Q7ZT14:
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor.
GN GHSR OR GHSRIA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Kidney, and Pituitary;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Wakita M., Shimada K.;
RT "Molecular characterization of chicken growth hormone secretagogue
RT receptor gene.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB095994; BAC76443.1; -.
DR EMBL; AB095995; BAC76444.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 347 AA; 39439 MW; 7A7543A9A94222P4 CRC64;

Query Match 39.4%; Score 849; DB 13; Length 347;
Best Local Similarity 46.7%; Pred. No. 4.4e-63;
Matches 164; Conservative 70; Mismatches 69; Indels 48; Gaps 6;

QY 33 FPLGALVPVAVCLCLFVVGSGNVVTVMLIGRYDMRTTNLYLGSMAVSDLLILIGLP 92
Db 19 FPAPVLTGITVACVLLFVVGVLGNLMTLVVSRFRDMRTTNLYLSSMAVSDLLILIGLP 78
QY 93 FDLVLRWRSPVWFGPLLRLSLSYVGEQCTYATLLHMTALSVERYLAICRPLARVLVTR 152
Db 79 LDLFELWQYRPNWFGDLLCKLPQFISECTYSTIINITALSVERVVALCFPLRAKVIITK 138
QY 153 RRVRLIALIWMALVALLSAGPFLVGVQDPGIVSVVPGNGTARIASSPPLWLSR 212
Db 139 RKVKLVILWAVSFISAGPIFVLGVGHE-----NGT-----NPLSTN----- 177
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QY 213 APPSPSPGPTABAAALFSRECRSPAQL--GALRVMLWVTTAYEFLPFLCLSLYLGLI 270
Db 178 -----ECRATEVAIRSGLLTMMVSISSIFFLPVFLVLLVSLI 216
QY 271 GRELWSSRRPLRGPAASGRGRHQTKRVLLVVVLAFTICLWLPFHVGRRIIYINTEDS--- 327
Db 217 GRKLWRRKRKNIGPSTIIRDKNNQTKVLMVVVVFATILCWLPFHVGRYLSKSPFAGSL 276
QY 328 RMVFSQYFNIVALQLFVLSASINPILYNLSKKYRAAFAKLLARKSRPR 378
Db 277 EIAVISQYCNLVSVFLVFLYSAINPILYNIMSKYRVAACR-LFGLKALPK 326

RESULT 4
O93412 PRELIMINARY; PRT; 374 AA.
AC O93412;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Orphan G protein-coupled receptor.
OS Spherooides nephelus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Spherooides.
OX NCBI_TaxID=39110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092336; PubMed=10628755;
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,
RA Patchett A.A., Howard A.D., Smith R.G.
RT "Ligand activation domain of human orphan growth hormone (GH)
RT secretagogue receptor (GHS-R) conserved from pufferfish to humans."
RT Mol. Endocrinol. 14:160-169(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF082209; AAC33472.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS00043; HTH_CNTR_FAMILY; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 374 AA; 42324 MW; 2CF9304F004C7A16 CRC64;

Query Match 39.2%; Score 845; DB 13; Length 374;
Best Local Similarity 45.5%; Pred. No. 1e-62;
Matches 187; Conservative 64; Mismatches 102; Indels 58; Gaps 12;

QY 5 WNGS-DSDEGAREPWPALPCDERRCSPPFALGVPTAVCLFVVGSGNVVWMLI 63
Db 13 WEGSHNGTAGLELP-----LNYSIPLAVITACTVLFTVVGSGNVWMLIV 61
QY 64 GRYDMRTTNLYLGSMAVSDLLILLGLPFLYRLSRPWPVGEPLLCRLSLYVGECTY 123
Db 62 SRYDMRTTNLYLCSMAVSDLFIFVCMPLDLYRWRYPWRFGDALCKLQFVSECTY 121
QY 124 ATLLHMTALSVERYLAICRPLARLVTRRRVRLIAVLWAVALLSAGPFLFVGEQDP 183
Db 122 STILCITALSVERYLAICFPLRAKALVTKRVRALLILLWTVLSLSAGPVMVGVKDS 181
QY 184 GISVVPGLNGTARIASSPL-ASSPPLMLSRAPPPSPGPTABAAALFSRECRPS--PA 240

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Db 182 --IMFPN-----SSDLNESSWPL-----EAVDTRECRMTQAV 212
QY 241 QLGAIRVMLWVTTAYEFLPFLCLSLYLGLIGRELWSSRRPLR-GPAASGRGRGRHQTKRV 299
Db 213 ESGLMEAMVWSSVFFMPFVCLTVLYGLIGRLWLRHRETTINSRVAYRDKSNRQIKM 272
QY 300 LVVVLAFTICLWLPFHVGRRIIYINTEDS---RMVFSQYFNIVALQLFVLSASINPILYN 356
Db 273 LVVVLAFTICLWLPFHVGRYLPQRLSDAPSLLSLLSEYCSLVSFVFLYLSAANPILYN 332
QY 357 LIISKYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGDTGVGTSTAN 407
Db 333 TMSWKIRGAVARLEFVSDSPFQ---RCR-TASTVKMD-----GWTESTVS 373

RESULT 5
O8MHZ5 PRELIMINARY; PRT; 366 AA.
AC O8MHZ5;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ghrelin/growth hormone secretagogue receptor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1, 2, and 3; TISSUE=Pituitary;
RA Murata T., Ikegami R., Morita Y., Shinozaki K.;
RA "Sheep Ghrelin/Growth Hormone Secretagogue Receptor.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY093948; AAM19733.1; -.
DR EMBL; AY093949; AAM19734.1; -.
DR EMBL; AY093950; AAM19735.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 366 AA; 41486 MW; 2F276651BC6C5D57 CRC64;

Query Match 38.0%; Score 819.5; DB 6; Length 366;
Best Local Similarity 42.1%; Pred. No. 1.4e-60;
Matches 175; Conservative 62; Mismatches 114; Indels 65; Gaps 8;

QY 5 WNGSDGPE-----GAREPWPALPCD-----ERRCSPPFALGVPTAVCLFVVGSGN 56
Db 2 WNAIRSELGNLTLPLDLDWAAPDNDLSLTDELPLFPAPLLAGVTATCVALFVVGAGN 61
QY 57 VTVVMLIGRVDMRTTNLYLGSMAVSDLLILLGLPFLYRLWSPWPVGFPLCRLSLY 116
Db 62 LLTMLVYSRPRELRTTNLYLSSMAFSDLLITFLCMLDLVRLMHYRPWNLDLCKLPQF 121
QY 117 VGECTYATLLHMTALSVERYLAICRPLARLVTRRRVRLIAVLWAVALLSAGPFL 176
Db 122 VSSCTYATLLHMTALSVERYLAICFPLRAKALVTKRVRALLILLWTVLSLSAGPFL 181
QY 177 VGVQDQPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTABAAALFSRECR 236
Db 182 VGVHE-----NCT-----DPRD-----TNECR 199
QY 237 PS--PAQLGALRVMLWVTTAYEFLPFLCLSLYLGLIGRELWSSRRPLRGPAASGRGRH 294
Db 200 ATEFAVRSGLITIMVWVSSIFFFLPFLVCLTVLYSLIGRLWRRRRSRVWVGASLRDQNH 259

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QY 295 QTKRVLVVVLAFLICWLPHVGRILYINTEDS---RMVFQSYFNIVALQIFYLASIN 351
Db 260 QTVKMLAVVFAFVLCWLFPHVGRYLFKSFPGSVIEIAQISQYCNLVFLFYFSAALN 319
QY 352 PIIYNLISKYRAAEPKLLARKSRGHRSDTAGEVAGDTGGTVGYTETSAN 407
Db 320 PIIYNIMSKYIRVAVFKLLGFEPFSQKSTLKDESSR-----AWTESSIN 365

RESULT 6
Q72ZJ9 PRELIMINARY; PRT; 331 AA.
AC Q72ZJ9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type 1a variant.
GN GHSRLV
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Pituitary.
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Wakita M., Shimada K.;
RT "Molecular characterization of chicken growth hormone secretagogue
receptor gene.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB095996; BAC76445.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 331 AA; 37567 MW; 1BE477BF2D7A3BEB CRC64;

Query Match 34.9%; Score 753; DB 13; Length 331;
Best Local Similarity 43.0%; Pred. No. 4.7e-55;
Matches 151; Conservative 68; Mismatches 68; Indels 64; Gaps 7;

QY 33 FPLGALVPVAVCLCLFVVGVSGNVVTVMILGRYDMRTTNTLYLGSMAVSDLLILGLP 92
Db 19 FPAVLITGITVACVLLFVVGVLGNLTMLVSRFRDMRTTNTLYLSSMAFSDLLIFLCP 78
QY 93 FDLRLWRSPWVFGPILCLSLYVGEGETYATLLHMTALSVERYLAICRPARVLVTR 152
Db 79 LDFRLWQYRPNFNGDLCKLFQFISECTSTILNITALSVERYVAICFPLRAKVIITK 138
QY 153 RVRRLIALVMAVALLSAGPFLFVGVQDPGISVVPGLNGTARIASSPLASPPILWLSR 212
Db 139 RKVKLVILLIWAIVSFISAGPIFVLGVGVEHE-----NGT-----NPLSTN----- 177
QY 213 APPSPSPGPETAFAALFSRECRSPAQL--GALRVMLWVTYAFFFLCLSLYGLI 270
Db 178 -----ECRATEYAIRSGLLTIMWISSIFFFLPVFCLTVLYSLI 216
QY 271 GRELWSSRPLRGPAAAGRGHRGRTKQVLLVVVLAFLICWLPHVGRILYINTEDS--- 327
Db 217 GRKLWRKKNKNGTIPSTIIRDKNNKQTVKMLGMAPPALCLQVRVLVC 262

RESULT 7
Q72ZJ8 PRELIMINARY; PRT; 267 AA.
AC Q72ZJ8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type 1b.
GN GHSRLB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Pituitary.
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Wakita M., Shimada K.;
RT "Molecular characterization of chicken growth hormone secretagogue
receptor gene.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB095997; BAC76446.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 267 AA; 30209 MW; 00563690B35AD107 CRC64;

Query Match 29.5%; Score 637; DB 13; Length 267;
Best Local Similarity 43.0%; Pred. No. 2e-45;
Matches 123; Conservative 58; Mismatches 55; Indels 50; Gaps 5;

QY 33 FPLGALVPVAVCLCLFVVGVSGNVVTVMILGRYDMRTTNTLYLGSMAVSDLLILGLP 92
Db 19 FPAVLITGITVACVLLFVVGVLGNLTMLVSRFRDMRTTNTLYLSSMAFSDLLIFLCP 78
QY 93 FDLRLWRSPWVFGPILCLSLYVGEGETYATLLHMTALSVERYLAICRPARVLVTR 152
Db 79 LDFRLWQYRPNFNGDLCKLFQFISECTSTILNITALSVERYVAICFPLRAKVIITK 138
QY 153 RVRRLIALVMAVALLSAGPFLFVGVQDPGISVVPGLNGTARIASSPLASPPILWLSR 212
Db 139 RKVKLVILLIWAIVSFISAGPIFVLGVGVEHE-----NGT-----NPLSTN----- 177
QY 213 APPSPSPGPETAFAALFSRECRSPAQL--GALRVMLWVTYAFFFLCLSLYGLI 270
Db 178 -----ECRATEYAIRSGLLTIMWISSIFFFLPVFCLTVLYSLI 216
QY 271 GRELWSSRPLRGPAAAGRGHRGRTKQVLLVVVLAFLICWLPHVGRILYINTEDS--- 310
Db 217 GRKLWRKKNKNGTIPSTIIRDKNNKQTVKMLGMAPPALCLQVRVLVC 262

RESULT 8
Q93414 PRELIMINARY; PRT; 559 AA.
AC Q93414;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orphan G protein-coupled receptor.
OS Spherooides nephelus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Spherooides.
OX NCBI_TaxID=39110;
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RN  SEQUENCE FROM N.A.
RX  MEDLINE=20092336; PubMed=10628755;
RA  Palya O.C., Feighner S.D., Fan C.P., McKee K.K., Hreniuk D.L.,
RA  Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,
RA  Patchett A.A., Howard A.D., Smith R.G.;
RT  "Ligand activation domain of human orphan growth hormone (GH)
RL  secretagogue receptor (GHS-R) conserved from pufferfish to humans.";
RL  Mol. Endocrinol. 14:160-169(2000).
DR  EMBL; AF082211; AAC33474.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODOPS.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
SQ  SEQUENCE 559 AA; 61956 MW; APB9F35FAF0CD5F6 CRC64;

Query Match 27.9%; Score 602; DB 13; Length 559;
Best Local Similarity 29.5%; Pred. No. 3.9e-42;
Matches 155; Conservative 65; Mismatches 125; Indels 180; Gaps 12;

QY 22 LPDCDERRC---SPFPLGALVPVAVCLCLFVVGSGNVVTVMLIGRYDMRTTNNLYLG 78
DB 20 LHKCSQGECHWEFV-FGMVUCVTIIVPLMFLGLNLTILVWVRPWRSTYDLS 78
QY 79 SMAVSDLLILGLPFDLYRLWRSPRVFGLPCLRLSLVYGEGETYATLLHMTALSVERYL 138
DB 79 SLAVSDILILLPLVDLYKLRWPPEFGEIFCKSTWFFSECCFTCSILHITISLERYL 138
QY 139 AICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLFVGVE-----ODPGIS 186
DB 139 AVCWPFATAKTVTRRTTIIIGCIWLGAALISAAPVWVVGVEEQSDQSLSGRESGAW 198
QY 187 -----VTPGL----- 191
DB 199 TGKEGKGFIFGERENRDKGLKDEOLEWNWKDEKMGCKNGVTKFGKGDKSLEV 258
QY 192 -NGTARIASSPLSLWLSRAPPSPGPE-----TAEAAALFSRECRPS--PAQLGA 244
DB 259 GEGTKEQEHGEEAAGEAQAQNKEDGEGGEGEDTDGGRMQVDTRCCRTDYAVSSGL 318
QY 245 LRYMLWTTAYFPLPFLCLSLYLIGRELWSSRPPLRGPAASGREHGRQTKRVLLVVV 304
DB 319 LSAMLVLSNMYFLVPLCLGLVGLIGRTLW-----LRS-QISRRDYNRRNTVMKLGVI 372
QY 305 LAPTIICMLPHVGRRIY-----INTE-----DSR----- 328
DB 373 LVFVLCWLPFHVGRITPFFSLGSDRPGVNSHALDSRVPLELPPPGALGESDEAAGDAF 432
QY 329 ----- 328
DB 433 SEAQTRGDGGRVLDTRGTARSDEGAAGPSTPEATTADPYDAENSTPLDTHSHQYF 492
QY 329 MMYFSQYFNVALQLFVLSASINPILYNLSKKYRAAFAKLLAR 373
DB 493 LYLVSQYFNLSVFLVLSAAINPLLYNLSERYRHAVHSLPRR 537

RESULT 9
Q8NE20
ID Q8NE20 PRELIMINARY; PRT; 426 AA.
AC Q8NE20;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein-coupled receptor 66.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
RN  SEQUENCE FROM N.A.
RP  TISSUE=Testis;
RA  Strausberg R.;
RL  Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC036543; AAH36543.1; -.
DR  Genew; HGNC:4518; GPR66.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0001607; F:neuromedin U receptor activity; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  InterPro; IPR005390; NeuromedinU.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODOPS.
DR  PRINTS; PR01565; NEUROMEDINUR.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
SQ  SEQUENCE 426 AA; 47322 MW; 7BFEB5DE2E2DC686 CRC64;

Query Match 22.6%; Score 486.5; DB 4; Length 426;
Best Local Similarity 33.7%; Pred. No. 1.4e-32;
Matches 129; Conservative 64; Mismatches 123; Indels 67; Gaps 10;

QY 39 VPVAVTAVCLCLFVVGSGNVVTVMLIGRYDMRTTNNLYLGSMAVSDLLILL-GLPFDLYR 97
DB 61 MPICATVLLIFVVGAVNGGLTCLVILRHKAMRPTNVYLFSLAVSDLLVLLVGLPLELYE 120
QY 98 LKRSRWVWGPPLLCRLSLVYGEGETYATLLHMTALSVERYLACRPLRARVLVTRRRVRA 157
DB 121 MWHNYPFLLVGGCYFRTLLFEMVCLASVLNLTALSVERYVAVVHPVLPQARSMVTRAHVR 180
QY 158 LIAVLWAVALLSAGPFLFVGVEODPGISVVGNGTARIASSPLSLWLSRAPPS 217
DB 181 VLGAWGLAMCLSLPNTSLHGIQO---LHV----- 207
QY 218 PPSGPTATAAAALFSRECRPSPAQLGALRVMLWTTA--YFFLPFLCLSLYLIGRELW 275
DB 208 PCRGPVDSAVCMVLRP-----RALYNVQTTALLFFCLPMAIMSVYLLIGLRLR 259
QY 276 SSRRLP-----RGPAA-----GRGRHGRQTKRVLLVVVLAFLICWLPHVGRRII 320
DB 260 RERLLMQEAKGRGSAARSRYTCRLQHDGRGRQVTKMLFVLVWVVGICWAPFHADRV 319
QY 321 Y--INTEDSRMMYFSQYFNVALQLFVLSASINPILYNLSKKYRAAFAKLL-----LARK 374
DB 320 WSVSWQNTDGLHLAFQHVHVISGIFFLGSAANPVLVLSMSSRFRTFQEQALCLGACCH 379
QY 375 SRPR--GFHRSRDTAGEVAGDTG 395
DB 380 LRPRHSHSLSRMTTGTSLCDVG 402

RESULT 10
Q9HB89
ID Q9HB89 PRELIMINARY; PRT; 426 AA.
AC Q9HB89; O43664;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuromedin U receptor 1 (Orphan G protein-coupled receptor) (GPR66)
DE protein).
DE NMUR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;

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DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 395 AA; 44844 MW; 0BB540024566903D CRC64;
 Query Match 22.1%; Score 475.5; DB 11; Length 395;
 Best Local Similarity 30.6%; Pred. No. 1.1e-31;
 Matches 115; Conservative 79; Mismatches 101; Indels 81; Gaps 11;

QY 30 CSPFPLGALVPVAVCLCLFVVGSGNVVTVMLIGRYDRMTTNNLYLGSMAVSDLLI-L 88
 DB 29 CGPKRSDLSPLSVVYALIFVVGVIQNLVCLVIARHQTLPNTNYLFLSLAVSDLLVLL 88
 QY 89 LGPFDFLYLWRSPWVFGPGLLCRLSLYVCGEGCTYATLLHMTALSVERVLAICRPLRARV 148
 DB 89 LGMPLEVEYLWHNYPLFGVGCYFXTALFETVCFASILSVTSIERYVAIVHPFRKL 148
 QY 149 LVTRRRVRALIAVLMAVALLSAGPFLVGV--EQDPGISVVGNGTARIASPLASSP 206
 DB 149 ESTERRALRLSLVMSFVSFSLPNTSIHGKIQQFPNGSVFG-----SATCTVTK 200
 QY 207 PLWLSRAPPPSPGPTAEAAALFSRECRPSAQLGALRVMLVTVTAYFF-LPFLCLSI 265
 DB 201 PMWV-----YNFIIQATSFLEYILPMTLISV 226
 QY 266 LYGLIGREL-----WSSRRPLRGPAASGRGRHRTQKRVLLVVLVAFIICWLP 313
 DB 227 LYILMGLRLKRDSELEADKVTVNIHRPSR-----KSVTKMLFVLVLFVFAICWTP 275
 QY 314 FHVGRITIIYNTDSRMVYFSQYFN---IVALQLFYLGSINPIILYNLISKYRAAFAKLL 370
 DB 276 FHVDR-LFFSFVDWETESLAAVENLIHVSGVFFYLSAVNPIIYNLLSRRFR-AAFRNV 333
 QY 371 LA-----RKSRPRG 379
 DB 334 VSPCKWCHPQHRPQG 349

RESULT 13
 Q96AM5 PRELIMINARY; PRT; 415 AA.
 ID Q96AM5 PRELIMINARY; PRT; 415 AA.
 AC Q96AM5; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Neuromedin U receptor 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; BC016938; AAH16938.1; -.
 DR Genew; HGNC:16454; NMU2R.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001607; F:neuromedin U receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR005390; NeuromedinU.
 DR InterPro; IPR005392; NeuromedinU2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01565; NEUROMEDINUR.
 DR PRINTS; PR01567; NEUROMEDINUR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 415 AA; 47770 MW; 30BFEDD706436AB9 CRC64;

RESULT 12
 Q8BZ39 PRELIMINARY; PRT; 395 AA.
 ID Q8BZ39 PRELIMINARY; PRT; 395 AA.
 AC Q8BZ39; 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Neuromedin U receptor type 2.
 GN NMU2R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT 60,770 full-length cDNAs.;
 RL Nature 420:563-573(2002).
 DR EMBL; AK036756; BAC29564.1; -.
 DR MGD; MGI:2441765; Nmu2r.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001607; F:neuromedin U receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR005390; NeuromedinU.
 DR InterPro; IPR005392; NeuromedinU2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01565; NEUROMEDINUR.
 DR PRINTS; PR01567; NEUROMEDINUR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.


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Query Match      22.0%; Score 475; DB 4; Length 415;
Best Local Similarity 30.8%; Pred. No. 1.3e-31;
Matches 115; Conservative 78; Mismatches 98; Indels 82; Gaps 12;

QY 30 CSPFPLGALVPVAVCLCLFVVGVSGNVVTVMLIGRYDMRTTNLYLGSMAVSDLLI-L 88
DB 37 CGPRRSHPFLPVSVVVPFVVGVLGVNLVCLVLQHQAMKTPNTYFLSLAVSDLLVL 96

QY 89 LGLPDLVLMRSRNPVPGPLICRLSLYVGECTYATLLHMTALSVERYLACRPLARV 148
DB 97 LGMPLEVVEMWNYFELFGPVGCYFKTALFETVCFASILSITTVSVERVAILHPFRKL 156

QY 149 LVTRRRVRLIALVMAVALLSAGPFLFVGVE--QDPGISVVPGLNGTARIASSPLASP 206
DB 157 QSTRRRALRILGVWGFSLFSLPNTSIHGKHFHFPNGSLVFG-----SATCTVIK 208

QY 207 PWLGRAPPPSPSGPETAABAAALFSRECRPSPAQIGALRVMLVWTVTAYFF-LPFLCLSI 265
DB 209 PMWI-----YNFIIQVTSFLFYLLPMTVISV 234

QY 266 LVCLIGRELWSSR-----RPLRGPASGRGRHQTRKRVLLVVLAFIICWLP 313
DB 235 LYYLMAIRLKOKSLEADGNANIQRPCR-----KSVNKMFLVLVFAICWAP 283

QY 314 FHVGRITTYINTED-SRMVYFSQVFNIVAL---QLFYLSASINPILYNLISKKYRAAFKL 369
DB 284 FHIDRLFFSFEWESES--AAVFNLVHVVGFFYLSSAVNPIIYNLLSRRFQ-AAFQN 340

QY 370 LLARKSRPRGFHR 382
DB 341 VLS-----SPHK 347

RESULT 14
Q9GZQ4 PRELIMINARY; PRT; 415 AA.
ID Q9GZQ4 Q9NRA6;
AC Q9GZQ4; Q9NRA6;
DT 01-WAR-2001 (TREMELrel. 16, Created)
DT 01-WAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Neuromedin U receptor 2 (Neuromedin U receptor-type 2) (G protein-
DE coupled receptor TGR-1).
GN NMUR2 OR NMUR2 OR TGR-1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20490668; PubMed=10899166;
RA Raddatz R., Wilson A.E., Artyemyehyn R., Bonini J.A., Borowsky B.,
RA Boteju L.W., Zhou S., Kouranova E.V., Nagorny R., Guevarra M.S.,
RA Dai M., Lerman G.S., Vayase P.J., Brancheck T.A., Gerald C., Forray C.,
RA Adam N.;
RT "Identification and Characterization of Two Neuromedin U Receptors
RT the Centrally Expressed in Peripheral Tissues and the Central Nervous
RT System."
RL J. Biol. Chem. 275:32452-32459 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11010960;
RA Shan L., Qiao X., Crona J.H., Behan J., Wang S., Laz T., Bayne M.,
RA Gustafson E.L., Monsma F.J. Jr., Hedrick J.A.;
RT "Identification of a Novel Neuromedin U Receptor Subtype Expressed in
RT the Central Nervous System."
RL J. Biol. Chem. 275:39482-39486 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11010960;
RA Pang L., Wang S., Laz T., Hedrick J.A.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 4-415 FROM N.A.
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MEDLINE=20351041; PubMed=10894543;
Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X.-M.,
Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B.,
Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., McKee K.K.,
Hreniuk D.L., McDonald T.P., Lynch K.R., Evans J.F., Auscine C.P.,
Caskey T., van der Ploeg L.H.T., Liu Q.;
RT "Identification of receptors for neuromedin U and its role in
RT feeding."
RL Nature 406:70-74 (2000).
[5]
RN SEQUENCE OF 4-415 FROM N.A.
RP PubMed=10887190;
RX Hosoya M., Moriya T., Kawamata Y., Ohkubo S., Fujii R., Matsui H.,
RA Shintani Y., Fukusumi S., Habata Y., Hinuma S., Onda H., Nishimura O.,
RA Fujino M.;
RT "Identification and Functional Characterization of a Novel Subtype of
RT Neuromedin U Receptor."
RL J. Biol. Chem. 275:29528-29532 (2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF272363; AAG24794.1; -
DR EMBL; AF292402; AAG03064.1; -
DR EMBL; AF242874; AAF82755.1; -
DR EMBL; AB041228; BAB13721.1; -
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
DR GO; GO:0001607; F: neuromedin U receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007267; F: cell-cell signaling; TAS.
DR GO; GO:0007417; F: central nervous system development; TAS.
DR GO; GO:0007631; F: feeding behavior; TAS.
DR GO; GO:0007186; F: G-protein coupled receptor protein signaling.; IEA.
DR GO; GO:0007218; F: neuropeptide signaling pathway; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR005390; NeuromedinU.
DR InterPro; IPR005392; NeuromedinU2.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PRINTS; PRO1565; NEUROMEDINUR.
DR PRINTS; PRO1567; NEUROMEDINUR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 415 AA; 47725 MW; C2BACD84B313390F CRC64;

Query Match      22.0%; Score 474; DB 4; Length 415;
Best Local Similarity 30.8%; Pred. No. 1.5e-31;
Matches 115; Conservative 78; Mismatches 98; Indels 82; Gaps 12;

QY 30 CSPFPLGALVPVAVCLCLFVVGVSGNVVTVMLIGRYDMRTTNLYLGSMAVSDLLI-L 88
DB 37 CGPRRSHPFLPVSVVVPFVVGVLGVNLVCLVLQHQAMKTPNTYFLSLAVSDLLVL 96

QY 89 LGLPDLVLMRSRNPVPGPLICRLSLYVGECTYATLLHMTALSVERYLACRPLARV 148
DB 97 LGMPLEVVEMWNYFELFGPVGCYFKTALFETVCFASILSITTVSVERVAILHPFRKL 156

QY 149 LVTRRRVRLIALVMAVALLSAGPFLFVGVE--QDPGISVVPGLNGTARIASSPLASP 206
DB 157 QSTRRRALRILGVWGFSLFSLPNTSIHGKHFHFPNGSLVFG-----SATCTVIK 208

QY 207 PWLGRAPPPSPSGPETAABAAALFSRECRPSPAQIGALRVMLVWTVTAYFF-LPFLCLSI 265
DB 209 PMWI-----YNFIIQVTSFLFYLLPMTVISV 234

QY 266 LVCLIGRELWSSR-----RPLRGPASGRGRHQTRKRVLLVVLAFIICWLP 313
DB 235 LYYLMAIRLKOKSLEADGNANIQRPCR-----KSVNKMFLVLVFAICWAP 283

QY 314 FHVGRITTYINTED-SRMVYFSQVFNIVAL---QLFYLSASINPILYNLISKKYRAAFKL 369
DB 284 FHIDRLFFSFEWESES--AAVFNLVHVVGFFYLSSAVNPIIYNLLSRRFQ-AAFQN 340
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QY 370 LLARKSRPRGFR 382
Db 341 VIS-----SFHK 347

227 LYLMGLRLKROESLEANKVAVNIHRPSKSVTKMLFVLVLVFAICWTDPHVDLFFSFV 286
325 ED--SRMMYFSQYFNIVAIQLFYLSASINPILYNLISKKYRAAFKLLLA-----RKS 375
287 EEWTESLAAVFNLIHVSVGVFFYLSSAVNPITYNLLSRFR-AAFRNVVSPCKWCHPRH 345
376 RPEG 379
346 RPOG 349

Search completed: July 4, 2004, 03:10:21
Job time : 76 secs

RESULT 15

Q9JIB1 PRELIMINARY; PRT; 395 AA.
AC Q9JIB1;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Neuromedin U receptor 2.
GN NMU2R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=20351041; PubMed=10894543;
RA Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X.-M.,
Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B.,
Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., McKee K.K.,
Hreniuk D.L., McDonald T.P., Lynch K.R., Evans J.F., Austin C.P.,
Caskey T., van der Ploeg L.H.T., Liu Q.;
RA "Identification of receptors for neuromedin U and its role in
feeding";
RL Nature 406:70-74 (2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF242875; AAF82756.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001607; F:neuromedin U receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR005390; NeuromedinU.
DR InterPro; IPR005392; NeuromedinU2.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR01565; NEUROMEDINUR.
DR PRINTS; PR01567; NEUROMEDU2R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 395 AA; 44722 MW; 01D3765B5D5355C0 CRC64;

Query Match 21.9%; Score 472.5; DB 11; Length 395;
Best Local Similarity 30.5%; Pred. No. 1.9e-31;
Matches 111; Conservative 81; Mismatches 115; Indels 57; Gaps 9;

QY 30 CSPFPLGALVPTAVCLCLFVVGSGNVVTVMILGRYRDMETTNLYLGSMAVSDLLI-L 88
Db 29 CGPKRSDLSLPVSAYALIFLVGNGNLLVCMVIRHQTIKPTNYLFLSLAVSDLLVLL 88

QY 89 LGLPFDLYRLWRSPWVFGPPLLCRLSLYVGGCTYATLLHMTALSVRYLAICRPLRARV 148
Db 89 LGMPLEIYEMHNPFLPGVGYFKTALFETVCVFASILSVTVSVRYVAIVHPRAKL 148

QY 149 LVTRRRVALLAVLWALLSAGPFLVGV--EQDPGISVVPGLNGTARIASSPLASSP 206
Db 149 ESTRRALRILSLWSFWSFSLPNTSIHGKQHPNGSSVPG-----SATCTVTK 200

QY 207 PLWLSRAPPPSPGPETAEEAALFRRCRPSAQLGALRVLWLTWTAYFF-LPFLCLSI 265
Db 201 PMWV-----YNLIQATSEFLFYLPMTLISV 226

QY 266 LYGLIGRELWSSRRFLRGPASGRGRHQRT-KRVLLVVVLAFLICWLPFHVGRYIYINT 324
Db 266